

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 164310

TO: Jon E Angell

Location: 2d20 / 2c18

Friday, September 02, 2005

Art Unit: 1635

Phone: 571-272-0756

Serial Number: 09 / 972916

From: Jan Delaval

Location: Biotech-Chem Library

Remsen 1a51

Phone: 571-272-2504

jan.delaval@uspto.gov

Search Notes	
·	



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⊏	rom	•	

Chan, Christina

To:

Angell, Jon E; STIC-Biotech/ChemLib

Subject:

RE: RUSH Sequence Search Request 09/972,916

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841 Remsen, 3E89

-----Original Message-----

From:

Angell, Jon E

Sent:

Tuesday, August 30, 2005 11:24 AM

To:

Chan, Christina ·

Subject:

RUSH Sequence Search Request 09/972,916

I would like to request a RUSH sequence search because this case is an after final amended case that was forwarded to me 8/29/2005.

If approved, please forward the request to STIC and CC a copy to me, THANKS!

SEARCH REQUEST FORM

Scientific and Technical Information Center

Examiner#: 78697 Art Unit: 1635

Phone Number: 571-272-0756

Date: 8/30/2005

Serial Number: 09/972,916 (THULE et al.)

Mailbox & Bldg/Room Location: REMSEN 2C18

Results Format Preferred (circle): Paper

I would like to have a standard search of the nucleic acid databases including the pending applications databases (i.e., an interference search) performed using the following SEQ. ID NOs. from application: 09/972,916

SEQ ID NO: 1 (nucleic acid 51 nucleotides in length)

SEQ ID NO: 2 (nucleic acid 219 nucleotides in length)

SEQ ID NO: 3 (nucleic acid 270 nucleotides in length)

SEQ ID NO: 4 (nucleic acid 321 nucleotides in length) SEQ ID NO: 5 (nucleic acid 372 nucleotides in length) SEQ ID NO: 6 (nucleic acid 423 nucleotides in length)

Please note that the above sequence are gene expression regulatory sequences and the claims encompass nucleic acid sequences comprising any 1 or more of the above sequences.

STAFF USE-ONLY Searcher: Searcher Phone: 2- 3504 Date Searcher Picked up: 8 366 Date Completed: 572/05 Searcher Prep/Rev. Time: (5 Online Time:_

Type of Search

Interference:

_ Oligomer: Encode/Transl:

Structure#:_ Inventor:____ Litigation:_ Vendors and cost where applicable

DIALOG: QUESTEL/ORBIT:

LEXIS/NEXIS:_

SEQUENCE SYSTEM: _ & WWW/Internet: Other(Specify):

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Please contact me by phone or email if you have any questions.

Thanks,
Eric

9. Eric Augell

Art Unit 1635

Office: REMSEN 2D20

mailbox: REM 2C18

571-272-0756

STAFF USE ONLY

Searcher:
Searcher Phone: 2Date Searcher Picked up:
Date Completed:
Searcher Prep/Rev. Time:
Online Time:

endors and cost where applicable
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LEXIS/NEXIS:
SEQUENCE SYSTEM:
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Other(Specify):

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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
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219
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Copyright (c) 1993 - 2005 Compugen Ltd.
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SUMMAR
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The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growth

New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin liver cells.

'n

WPI; 2002-674190/72.

Thule PM;

(THUL/) THULE P M.

11-OCT-2000; 2000US-0239113P 10-OCT-2001; 2001US-00972916

Claim 8; Page 13; 37pp; English.

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ALIGNMENTS

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RESULT 1
ABX15372
ID ABX1
Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promotor; hyperglycaemia; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic; intracellular hormone receptor; insulin regulator construct; anabolic.
                                                                                                                                                                                                                                 08-AUG-2002.
                                                                                                                                                                                                                                                       US2002107198-A1.
                                                                                                                                                                                                                                                                              Rattus norvegicus.
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RESULT 2
ABX15373
ID ABX1
XX ABX1
AC ABX1
XX Gluc
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production, to modulate hyperglycaemia (without severe hypoglycaemia), to
cincrease fat catabolism and to retard protein catabolism. The construct
provides stimulation of insulin expression by glucose (but not other
carbohydrates) and glucocorticoids and inhibition by glucagon so that a
combination of these effects can maintain nearly euglycaemic conditions
cin diabetics during short-term fasting, large carbohydrate loads or when
cfed ad libitum and prevent pathological ketogenesis and ketoacidosis,
thus inhibiting the long-term complications of diabetes. The properties
cof the construct are essentially specific for hepatocytes and well-
cinhibition of cellular protein degradation, and inhibition, or
constructed the patoma lines and insulin expression in these cells may
chave effects additional to those provided by secreted insulin, e.g.
constituent of cellular protein degradation, and inhibition, or
constructed insulin-sensitive element of the invention
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Best Local S
Matches 219
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                                         Thule PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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intracellular
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Sequence

270

BP;

95 C;

65 G;

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Other;

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The invention relates to an insulin regulator construct comprising a CC glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene CC promoter and an insulin-sessitive element (ISE) of an insulin-like growth CC factor binding protein-1 (IGFBP-1) basal promoter. The construct is used CC to treat or prevent diabetic complications, to regulate insulin CC production, to modulate hyperglycaemia (without severe hypoglycaemia), to CC increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other CC carbohydrates) and glucocorticoids and inhibition by glucagon so that a CC combination of these effects can maintain nearly suglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when CC fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties CC differentiated hepatoma lines and insulin expression in these cells may CC inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence
                                       innibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat insulin regulator construct of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 13-14; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-674190/72
63 A;
47 T;
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Matches
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Best Local
232
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                                                                                                         112
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                                                                                                                                                                                                                al Similarity
219; Conserv
               AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC
                                                                      CCACTGCCCGACGACACACACACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
                                                                                                                         TCACAAGCAAAACAAACTTATTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA
                                                                                                         TCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA 111
AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC
                                                   CCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
                                                                                                                                                                                                               100.0%;
larity 100.0%;
Conservative 0
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                                                                                                                                                                                                                            Score 219; DB 6;
Pred. No. 2.7e-60;
                                                                                                                                                                                                                Mismatches
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                         219
                                                                                                                                                                                                                                        Length 270;
270
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                                                                                                         171
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ABX15374;
                   ABX15374 standard; DNA;
                     321
                     ВP
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Rat insulin regulator construct

DNA #2

17-APR-2003

(first entry)

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RESULT 3
ABX15374
ID ABX1
XX ABX1
XX ABX1
XX ABX1
XX Gluc
XX insu
XX i Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic; Synthetic Rattus norvegicus

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ABX15375
ID ABX1
XX ABX1
AC ABX1
XX DT 17-4
XX DE Rat
XX Gluc
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                                                                                                                                                                               RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucocorticoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may and effects additional to those provided by secreted insulin, e.g. stimulation of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat insulin regulator construct of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1;
                                 Rat insulin regulator construct DNA #3.
                                                                        17-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like gro
                                                                                                           ABX15375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
                                                                                                                                          ABX15375 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page 14; 37pp; English
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                                                                                                                                                                                                                                                                   181
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                                                                                                                                                                                                                                   283
                                                                                                                                                                                                                                                                                                                                                                                                                                                103
                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                      CCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC 180
                                                                                                                                                                                                                                                       AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC 219
                                                                                                                                                                                                                                                                                                    CCACTGCCCGCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                             TCACAAGCAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 BP; 77 A; 111 C; 84 G; 49 T; 0 U; 0 Other;
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                                                                        (first
                                                                      entry)
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Pred. No. 2.9e-60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an insulin regulator construct comprising a CC glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene CC promoter and an insulin-sensitive element (ISE) of an insulin-like growth CC factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin (CC production, to modulate hyperglycaemia (without severe hypoglycaemia), to cincrease fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other CC carbohydrates) and glucocorticoids and inhibition by glucagon so that a CC combination of these effects can maintain nearly euglycaemic conditions (combination of these effects can maintain nearly euglycaemic conditions (combination of these effects can maintain nearly euglycaemic conditions (combination of these effects can maintain nearly euglycaemic conditions (combination of the long-term complications of diabetes. The properties conditions inhibiting the long-term complications of diabetes. The properties conditions inhibition of cellular protein degradation, and inhibition, or inhibition of cellular protein degradation, and inhibition, or these catabonial to those provided by secreted insulin, e.g. catabonial to the catabonial to the
                                                                                                                                                                                                                                                                                                                                                                            Matches 219;
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 372 BP; 87 A; 128 C; 102 G; 55 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin liver cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page 14; 37pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represents a rat insulin regulator construct of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-674190/72.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hepatocyte; hepatoma; cellular protein degradation; antidiabetic; intracellular hormone receptor; insulin regulator construct; anabolic
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                181
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AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC
                                                                                                                                                                                                                        TCACAAGCAAAACTAATTTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA
                                                                  CCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
                                                                                                                   CCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
                                                                                                                                                                     TCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA
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Pred. No. 3e-60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the invention
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                  219
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                                                                                                                                                                                                                                                                                                                                                                         Gaps
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AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC 372

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ABX15376
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                                                                                                                                                                                                         Matches 219;
                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                     to treat or prevent diabetic complications, to regulate insuling production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucocorticoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growth factor binding protein-1 (IGFBP-1) basal promoter. The construct is used
                                                                                                                                                                                                     Sequence 423 BP; 81 A; 149 C; 116 G; 77 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; glucose; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 14; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-674190/72.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intracellular hormone receptor;
                                                                                                                                                    Local
                                                            205
                        61
                                                                                             Similarity
TCACAAGCAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA
                                                                                           TCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA
                                                                                                                                                                                                                                             a rat
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                                                                                                                                                                                                                                         insulin regulator construct of the invention
                                                                                                                                                                   100.
                                                                                                                                                    100.0%;
                                                                                                                                 <u>,</u>
                                                                                                                         Score 219; prod. No. 3.1e-60;
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                                                                                                                                                                   Length 423;
                                                                                                                                 Indels
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insulin;
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RESULT 6
ABK63701
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15-MAY-2001;
22-MAY-2001;
cells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the hepatotoxicity of a compound, comprising detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression. The method can also be used to identify an agent which modulates the toxic response and predict cellular pathways that a compound modulates in a cell. The methods utilise a set of at least two probes (on a solid support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer system comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification,
                                                                                                                                                                                                                                                     compounds or the progression of these global changes in gene expression in t
                                                                                                                                                                                                                                                                                                                                                                     Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cell exposed to the toxin and comparing these to gene expression in unexposed
                                                                                                                                                                                                                                     The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the global changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat sequence differentially expressed in response to a hepatotoxin #1608.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENE
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                                                                                                                                                                                                                                                                                                                        SEQ ID
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                                                                                                                                                                                                                                                                                                                                                           cells.
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2001US-0290029P.
2001US-0290645P.
2001US-0295336P.
2001US-0295798P.
2001US-0297459P.
2001US-0298884P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression; centrilobular necrosis; steatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001US-0303459P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0222040P
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                                                                                                                                                                                                                                                                                                                        NO 1608; 239pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                        English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Castle AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 423
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RESULT 7
ADB58201
ID ADB58201
ID ADB58201
ID ADB58201
ID O4-I
DT O4-I
DT O4-I
DT O4-I
DT O4-I
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XX TOX:
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Best Local S
Matches 77
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The present invention relates to a method for predicting a toxic effect of a compound. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising SEQ ID 1-4925, where differential expression of the gene indicates at least one toxic effect. The method is useful for predicting at least one toxic effect of a
                                                                                                                                                                                                              predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to
                                                                                                                                                                                                                                                                                                                                              Mendrick D,
                                                                                                                                                                                                                                                                                                                                                                                                                              11-JAN-2002; 2002US-00060087
15-MAR-2002; 2002US-0364045P
15-MAR-2002; 2002US-036405SP
30-DEC-2002; 2002US-0436643F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-2003
                                                                                                                                                    Claim 1; SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toxicity-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1500 BP; 336 A; 408 C; 380 G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003064624-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Toxic; toxin; gene expression profile; hepatotoxicity; liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB58201 standard; DNA; 1500 BP
                                                                                                                                                                                                                                                                                                                                                                                      (GENE-)
                                                                                                                                                                                                                                                                                                      2003-689530/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            screening;
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                                                                                                                                                                                                                                                                                                                                                                                        GENE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACTTCCGCTACTATCTA 85
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                                                                                                                                                                                                                                                                                                                                              Porter M,
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                                                                                                                                                                                                                                                                                                                                                                                        LOGIC
                                                                                                                                                    NO 3227; 1156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            toxicity assay; ds.
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98.7%;
                                                                                                                                                                                                                                                                                                                                              Johnson
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Pred.
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No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1500;
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                                                                                                                                                                                                                                                                                                                                              Elashoff M;
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RESULT 8
ADB52710
ADB52710
ADB52710
ADB52710
ACC ADB5
ACC ADB5
XXX ADB5
XXX Ucoxi
KW toxi
KW toxi
KW prim
XXX WO20
XXX WO20
XX WO20
XX WO20
ACC ADB5
ACC ADB
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Best Local
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                                                                                                                                                                                                                                                          19-APR-2002;
22-APR-2002;
08-MAY-2002;
09-MAY-2002;
09-MAY-2002;
                        Mendrick
Elashoff
                                                                                                                                                                                                                                                                                                                                                                                10-APR-2002;
11-APR-2002;
19-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              compound, predicting hepatotoxicity or the progression of a toxic effect of a compound, identifying an agent that modulates the onset or progression of a toxic response, predicting the cellular pathways that a compound modulates in a cell, and identifying an agent that modulates at least one activity of a protein. The method and compositions of the present invention using a database of genes having liver toxin-induced differential expression, are useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                09-MAY-2002;
09-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-APR-2002;
10-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-APR-2002;
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13-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
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77; Conserv
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                                                                                                                                                                                        2002US-0353171P
2002US-0363534P
2002US-037024B
2002US-0371134P
2002US-0371135P
2002US-0371159P
2002US-0371159P
2002US-0373601P
2002US-0373601P
2002US-0373601P
2002US-0378653P
2002US-0378653P
2002US-0378653P
2002US-0378653P
2002US-0378653P
2002US-0378653P
2002US-0378653P
2002US-0378653P
2002US-0378653P
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                                                 Porter M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
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                                                   Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85
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Pred. No. 3.6e-14;
D; Mismatches 1
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                                              Higgs
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                                                 В,
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                                                 Castle A,
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2003-731472/69

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RESULT 9
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Best Local S
Matches 77
01-NOV-2001;
21-NOV-2001;
06-DEC-2001;
19-DEC-2001;
                                                      10-JUL-2001;
28-AUG-2001;
27-SEP-2001;
22-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                                                                                                            19-JUN-2001;
10-JUL-2001;
                                                                                                                                                        22-MAY-2001;
13-JUN-2001;
                                                                                                                                                                                                                                                         WO200295000-A2
                                                                                                                                                                                                                                                                                                                               Toxic effect; gene expression profile; renal toxicity; toxicity marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
                                                                                                                                                                                                 22-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                        Toxicity modelling related rat gene SEQ ID No 1613.
                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                            ABT41911 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 44; SEQ ID NO 3252; 874pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1500
                                                                                                                                                                                                                                                                                                                drug
           1; 2001US-0292335P.
2001US-0297523P.
2001US-0298925P.
2001US-0303808P.
2001US-0303810P.
2001US-0315047P.
2001US-0324928P.
2001US-0324928P.
2001US-0330462P.
2001US-0331805P.
2001US-0331805P.
2001US-0331805P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                   2002WO-US016173
                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
                                                                                                                                                                                                                                                                                                               screening; toxicity assay; rat; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 A; 408
                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.9%;
98.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1500
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Pred. No. 3.6e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1500;
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                                                                                                               The invention relates to a novel method of predicting at least one toxic CC effect of a compound. The method comprises a gene expression profile of a CC tissue or cell sample exposed to the compound, and comparing the gene CC expression profile to a database compound, and comparing the gene CC information given in the specification. The methods are useful for CC predicting at least one toxic effect of a compound, predicting the CC progression of a toxic effect of a compound, predicting the renal CC conscity of a compound, or identifying toxicity markers in tissues or CC cells exposed to known renal toxin. The genes are useful as toxicity CC markers in drug screening and toxicity assays, in monitoring disease or CC physiological states, or disease progression. This polynucleotide CC represents a rat DNA sequence relating to the toxic effect database CC described in the specification. NOTE: The sequence data for this patent CC did not form part of the printed specification, but was obtained in CC electronic format directly from the World Intellectual Property
                                       Query Match
Best Local S
Matches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-FEB-2002;
21-FEB-2002;
21-FEB-2002;
15-MAR-2002;
08-APR-2002;
08-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-APR-2002;
17-APR-2002;
                                                                                                           Sequence 1500 BP; 336 A; 408 C; 380 G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page; 446pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 profile to a database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Predicting at least one toxic effect of a compound, useful for toxicity modeling, comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-148464/14.
                                         77;
                                                          Similarity
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2002US-0357843P.

2002US-0357844P.

2002US-0364134P.

2002US-0370144P.

2002US-0370206P.

2002US-037024P.

2002US-03772794P.

2002US-0371679P.
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porter M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOGIC
                                                        34.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnson K, Higgs B,
                                         <u>.</u>
                                                          Score 76.4; DB 10 Pred. No. 3.6e-14;
                                           Mismatches
                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Castle A,
                                                                           Length 1500;
                                           Indels
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                                       Gaps
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RESULT 10
ADP72689
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                                 dis; toxic effect; gene expression profile; kidney tissue; differential gene expression; toxicity progression; toxicity drug screening; toxicity assay; kidney pathology; nephritis; kidney necrosis; glomerular injury; tubular injury;
                                                                                 Renal toxin progression gene
                                                                                                                                          ADP72689
                                                                                                                                                                                                                                         197 CACTICCGCTACTAGCTA 214
                                                                                                                                                                                         83
                                                                                                                                                                                                                             8
                                                                                                                                          standard; DNA; 1500
                                                                                                                                                                                         CACTTCCGCTACTATCTA
                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                         85
                                                                                  marker #1278.
                                                                                                                                          ₿₽
                                                       toxicity
                                                       marker;
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Rattus norvegicus

focal segmental glomerulosclerosis

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RESULT 11
AAH22429
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          SEXEXEXEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC the invention relates to a method of predicting (the progression of) a CC toxic effect of a compound by preparing a gene expression profile of a CC kidney tissue or cell sample exposed to the compound and comparing the cCC gene expression profile to a database, or detecting the level of gene(s) CC differential gene expression compared to a control indicates a toxic ceffect (toxicity progression). The method is useful for predicting (the progression of) at least one toxic effect of a compound. The genes are CC useful as toxicity markers in drug screening and toxicity assays. The CC methods are useful for predicting the likelihood that a compound or test agent will induce various specific kidney pathologies, such as nephritis, CC kidney necrosis, glomerular and tubular injury, or focal segmental CC glomerulosclerosis. The methods are useful for determining the similarity of a toxic response to one or more individual compounds and for CC predicting or elucidating the potential cellular pathways influenced, CC induced or modulated by the compound or test agent. The kit is useful for predicting the progression of renal disease states, for identifying genes CC that show promise as new drug targets and for screening known and newly CC designed drugs. This sequence corresponds to a gene marker used in the CC form part directly from MIPO at fire with was obtained in electronic CC forms and directly from MIPO at fire with was obtained in electronic CC forms the compound of the invention. (Note: The sequence data for this patent did not forms part directly from MIPO at fire with a compound in the compound of the invention.
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Matches
Identification; toxic; hepatotoxic; differential non-steroidal antiinflammatory drug; ds.
                                                                                                                                                                                                                                                                                                              AAH22429 standard; DNA; 5001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1500 BP; 336 A; 408 C; 380 G; 376 T; 0 U; 0 Other;
                                                                                                             Rat insulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Predicting (the progression of) a toxic effect of a compound, for monitoring the progression of renal disease states, comprises preparing a gene expression profile of a kidney tissue or cell sample exposed to the
                                                                                                                                                                                                                                           AAH22429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mendrick DL,
Elashoff M;
                                                                                                                                                                            22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACTTCCGCTACTAGCTA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACAAACCCAGCGAGCATTGAACACTGCACAACGCCATCTGCCCAGAGAGCTGTGACCAC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACTTCCGCTACTATCTA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
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                                                                                                                                                                        (first entry)
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                                                                                                  growth factor binding protein nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 76.4;
Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                   gene expression; NSAID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1500;
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RESULT 12 ABN95896

ABN95896 standard; DNA; 6128

ВP

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61

CACTTCCGCTACTATCTA

78

13-AUG-2002

(first entry)

Gene #2394 used to diagnose liver cancer.

Homo sapiens

Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.

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                                                                                                                                                                                              The present invention describes a method of screening a test agent for CC hepatotoxicity. The method comprises: (a) providing a test cell copullation comprising a cell capable of expressing one or more nucleic acid sequences selected from the group consisting of RISKMARKER 1-8 and INJURYMARKER 1-10; (b) contacting the test cell population with a test center (c) measuring expression of one or more of the nucleic acid sequences in the test cell population; (d) comparing the expression of the nucleic acid sequence in the test cell population to the expression of the nucleic acid sequence in an reference cell population comprising at least one cell whose exposure status to a hepatotoxic agent in known; and (e) identifying a difference in expression levels of the RISKMARKER cor INJURYMARKER sequences, if present, in the test cell population and reference cell population. The method is useful for identifying a hepatotoxic agent. The present sequence is given in the exemplification of the patotoxic agent. The present sequence is given in the exemplification.
                                                                                                                     Matches
                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-NOV-1999;
18-FEB-2000;
20-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening hepatotoxic agent comprises contacting test cell population expressing RISKMARKER or INJURYMARKER with agent, comparing expression that reference population and identifying difference in expression with reference population and identifying difference in expression
                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                              of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 22-24; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            levels.
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              197
                                              1
                                                                                                                     77;
                                                                                                                                      Similarity
                                                                                                                                                                                          5001
CACTTCCGCTACTAGCTA 214
                                                                                  CACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCCAGAGAGCTGTGACCAC 196
                                                CACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCCAGAGAGCTGTGACCAC
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; 2000US-0183531P.
; 2000US-00717321.
                                                                                                                   Conservative
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                                                                                                                                                                                          BP; 1225 A; 1204 C; 1261 G;
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                                                                                                                                    34.9%;
                                                                                                                     0;
                                                                                                                Score 76.4; DB 4;
Pred. No. 5.3e-14;
0; Mismatches 1
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RESULT 13
ABV75371
ID ABV75
XX ABV75
XX ABV75
XX O7-M2
XX U7-M2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cyvostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                         Insulin-like growth factor binding protein; IGFBP; cytostatic; liver;
cancer; human; IGFBP-1; gene; ds.
                                                                                                                                                    Human IGFBP-1
                                                                                                                                                                                                             07-MAR-2003
                                                                                                                                                                                                                                                                       ABV75371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6128 BP; 1504 A; 1497 C; 1504 G; 1623 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing and detecting the progression carcinoma or metastatic liver tumor in a
      Homo sapiens
                                                                                                                                                                                                                                                                                                                           ABV75371 standard; DNA; 6128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 2394; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-426119/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGCATGGTCCACTGCCCGCGAGACACAAACCCCAGCGAGCATTGAACACTGC-ACACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCATCTGCCCAGAGAGCTGTGACCACCACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGCATCGGCCACCGCCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAACCTCCTGGTGCAAGTGGCGCGGCCTGTGCCCTTTATAAGGTGCGCGCTGTGTCCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCACCCTCCCAGAGAGCACTGGCCACCGCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                 gene
                                                                                                                                                                                                       (first entry)
                                                      IGFBP-1; gene; ds
                                                                                                                                                 sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 60.8;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATCCAGCGAGCATCTGCCGCCGCGCGCCGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vockley JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            676
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                                                                                                                  Matches
                                                                               Best Local
                                                                                        Query Match
                                                                                                                                     The invention relates to detecting the presence or diagnosing the risk of a liver cancer in a patient. The method involves detecting in a biological sample obtained from the patient aberrant expression of a gene encoding an insulin-like growth factor binding protein (IGBBP). The method is useful for detecting the presence or diagnosing the risk of a liver cancer or for screening agents in a patient. The agent is useful for the manufacture of a medicament for treating and/or preventing liver cancer. The present sequence represents a human IGPBP-1 polypeptide encoding genomic DNA (GenBank Accession No. M74587)
                                                                                                                Sequence 6128
                                                                                                                                                                                                                                                                                                                                                                                               (NACA-)
                                                                                                                                                                                                                                                      Example; Page 104-108; 142pp; English.
                                                                                                                                                                                                                                                                                       Detecting the presence or diagnosing the risk of a liver cancer in patient comprises detecting aberrant expression of a gene encoding
                                                                                                                                                                                                                                                                                                                           P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAY-2001;
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                                                                                                                                                                                                                                                                            insulin-like growth factor binding protein.
                        473
 62
                                              N
                                                                               Similarity
                                                                                                                                                                                                                                                                                                                           ABB82757.
                                                                                                                                                                                                                                                                                                                                                                                   SINGAPORE GEN HOSPITAL ARGAET V P.
                                                                                                                                                                                                                                                                                                                                                                                                        NAT CANCER CENT SINGAPORE PTE LTD.
  TAACCC---
                                             CACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCAT 61
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                2001US-0288441P
                                                                                                                BP; 1504 A; 1497 C;
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/*tag= f
/number= 3
4170. .5068
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/*tag= e
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/number= 1
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/*tag= d
/number= 2
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/product= "IGFBP-1"
/product= "insulin-like growth factor binding protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'number= 4
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/number= 3
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                                                                               27.8%;
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-GTGCTGCCGAGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAGC 111
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                                                                    °.
                                                                               Score 60.8; DB 10 Pred. No. 5.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                               PTE
                                                                     Mismatches
                                                                                                                1504 G;
                                                                                          DB 10;
                                                                                                                1623 T; 0 U; 0 Other;
                                                                     Indels
                                                                                          Length 6128;
                                                                   19;
                                                                    Gaps
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                        532
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GACAATCAT 61	2 CACAAGCAAAACATATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCAT	ş
14; 19; Gaps 3;	Query Match 27.8%; Score 60.8; DB 4; Length 6134 Best Local Similarity 66.5%; Pred. No. 5.9e-09; Matches 141; Conservative 0; Mismatches 52; Indels 1	Z B Q
ner;	Sequence 6134 BP; 1505 A; 1498 C; 1507 G; 1624 T; 0 U; 0 Othe	ő
ring of der where the thology	C gene profile can be used for diagnosis, prognosis or monitoring of C treatments and for investigating a predisposition to a disorder where the C gene is associated with a cancer, immunopathology or neuropathology	3222
order. The	to produce an expression profile that defines a metabolic developmental process, treatment, condition, disease or di	ដែកដ
(II) are used	embryonic stem cells into a tissue selected from brain, he liver, lung, skeletal muscle or pancreatic tissues. (I) ar	ត្រក់
lies or their pharmaceutical ptiation of	mimetics, peptides, proteins, agonists, antagonists, antik fragments, immunoglobulins, inhibitors, drug compounds and agonts. Exoression of (1) in a sample indicates the differ	หหห
. (I) and preening sic acids,	neuroprotective activities, and can be used in gene therag proteins (II) encoded by then are used in high throughput assays to select DNA molecules, RNA molecules, peptide nuc	កកក
/nucleotide	AAH57161 to AAH57576 represent cell and tissue specific posequences (I). (I) can have cytostatic, immunomodulatory a	ដែកទ
	Claim 1; Page 246-248; 327pp; English.	3 82 5
nosis, ne gene is	New cell and tissue specific polynucleotides useful for diagnos prognosis or monitoring of treatments for disorders where the gassociated with a cancer, immunopathology or neuropathology.	रेनेनेन
	WPI; 2001-291057/30.	€ ₩ 5
	Sornasse T, Seilhamer JJ, Watson GA;	RH S
	(INCY-) INCYTE GENOMICS INC.	× × ×
	04-NOV-1999; 99US-0163508P.	3 % 5
	02-NOV-2000; 2000WO-US030396.	3 43 5
	10-MAY-2001.	393
	WO200132927-A2.	2 Z S
	Homo sapiens.	ຂ జ :
uscle; lung; 88; modulatory; copathology.	Human; tissue specific; diagnosis; brain; heart; skeletal muscle; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss; metabolic disease; developmental disease; cytostatic; immunomodula neuroprotective; gene therapy; cancer; immunopathology; neuropatho	85555
	Human liver cell specific cDNA sequence SEQ ID NO:329.	28
	10-SEP-2001 (first entry)	243
	AAH57489;	ຂີດ:
	RESULT 14 AAAH57489 AA AAH57489 standard; cDNA; 6134 BP.	RESU
	645 CCACCCTCCCAGAGAGCACTGGCCACCCTCC 676	용
	171 CCATCTGCCCAGAGAGCTGTGACCACCACTTC 202	ş
	593 GAGCATCGGCCACCGCCATCCCATCCAGCGAGCATCTGCCGCCGCGCCG	용
17	12	ş
	533 TAACCTCCTGGTGCAAGTGGCGCGCGCTGTGCCCCTTTATAAGGTGCGCGCTGTGTCCAGC	မှ

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RESULT 15
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ID ABL32
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Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                        The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2997/c
ABL32997
                                                                                                                                                                                                                                                                      Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antiporiatic; antainflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                             Sequence
                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 970; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                         WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                                                                                                      Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune system associated gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 CAGCATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGC-ACACGG 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                             7061 BP; 1852 A; 147 C; 1865 G; 3197 T;
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                                                                                                                                                                                                                                                                                                                                                                       Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; DNA; 7061
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17.3%;
ilarity 73.8%;
Conservative
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2000DE-01043826.
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                                                                                                                                                                                                                                                                                                                                                                         Berlin
Score 37.8; DB 6;
Pred. No. 0.16;
0; Mismatches 17;
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                              Length 7061;
                                                               0 U; 0 Other;
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2 CACAAGCAAAACATATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCAT 61

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Indels

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Result
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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       Pred. No.
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-945-140-2
US-08-975-428-1
US-09-949-016-13508
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17201, Appli
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RESULT 1 US-08-945-140 US-08-945-140 US-08-945-140 US-08-945-140 US-08-945-140 US-08-945-140 US-08-945-140 US-08-945-140 US-08-945-140	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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1, Application 2, 6309878 100000000000000000000000000000000000	44444444444333 22222222222222333 44447777777777
Application US/089451 3309878 COMMATION: CHEN, Ruihuan F: CHEN, Ruihuan F: CHEN, Ruihuan F: KAHN, Axel INVENTION: GLUCOSE-I INVENTION: VECTOR 7 SEQUENCES: 10 VENCE ADDRESS: BE: Rhone-Poulenc Ro 500 Arcola Road, Ma Collegeville PA SEQUENCES: 10 VENCE ADDRESS: E PALEDIALE FORM: TYPE: Floppy disk TYPE: Floppy disk TYPE: Floppy disk TYPE: PC-DOS/MS RE PALEDIAN Release RPPLICATION NUMBER: PC-DOS/MS RE PALEDIA NUMBER: US/08/9 DATE: 11CATION NUMBER: WO PCT/ VIION NUMBER: WO PCT/ VIION NUMBER: 29,699 ACTION NUMBER: 20,699 ACTION	1257 1472 41522 41523 601 798 1314 1716 4250 14570 14570 14570 601 389504 601 601 930 1980 8392
US/089451 huan runo GLUCOSE-II VECTOR 10 S: Road, Ma Rouperine Relase: ATA: US/08/9- AR-1995 A	4444444444
.NDUC .NDUC 	US-09-82 US-09-94 US-09-94 US-09-94 US-09-95 US-09-95 US-09-90 US-09-90 US-09-90 US-09-90 US-09-90 US-09-94
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	452, App 1388, Ap 11932, A 13744, A 11759, Ap 11608, A 2799, Ap 11012, App 11012, App 1101

Query Match

100.0%;

Score 51;

DB 3;

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US-08-791-849A-14
                                                                US-08-791-849A-14
 Query Match
Best Local Similarity
Matches 51; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08791849A Patent No. 5914449 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 13011 base pai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: January CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,849A
                                                                                                                         FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskett
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
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ADDRESSEE: Wenderoth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                                                                                                    FEATURE:
NAME/KEY:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                    LOCATION:
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DEDNESS: double
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805 Fifteenth Street, N.W., #700
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NVENTION: Method for Increasing Storage
NVENTION: Lipid Content in Plant Seed
 100.0%; ilarity 100.0%; Conservative 0
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                                                                           join(3219..3765, 3949..5916, 6009..6151, 6284..6417, 6605..6920, 7191..7301, 7453..7664, 7818..7910, 8078..929. 9480..10162)
                                                                                                                                                                                                                   join(3212..3218, 3766..3948, 5917..6008, 6152..6283, 6418..6604, 6921..7191, 7302..7452, 9298..9479, 10163..10269)
                                                                                                                                                                                                                                                                                            rat (Rattus norvegicus)
                                                                                                                                                                                                                                                                                                                                                           linear
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6152..6283, 6418..6604, 6921..7191, 7302..7452,
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US-09-949-016-11786
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Patent No. 6812339
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                                                                                                                                                                                                                                 PRIOR FILING DATE: 200 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                      TYPE: DNA ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 207012
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les 39; Conserv
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39; Conser
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                                                                                           71.8%;
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17205
LENGTH: 15108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11786
LENGTH: 15108
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PRIOR PRICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
2357 CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCTGGCATA 2399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2357 CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCTGGCATA 2399
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o. 6812339
                               9 CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCCAGTGTA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cacegeecacrecereerrecreeacrereecececaerera 51
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                                                                                                                                               Score 36.6; DB 4; Length 15108; Pred. No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36.6; DB 4
Pred. No. 0.0012;
0; Mismatches
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; LOCATION: (0)...(0)
; OTHER INFORMATION: Zic 1 Protein gene; Genbank Acession D76435
US-09-234-332-5
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US-09-234-332-5
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APPLICANT: Cedars-Sinai Medical Center

APPLICANT: Michel F. Levesque, M.D.

APPLICANT: Michel F. Levesque, M.D.

APPLICANT: TOOMAS Meuman, Ph.D.

TITLE OF INVENTION: CONVERSION OF NON-NEURONAL CELLS INTO

TITLE OF INVENTION: NEURONS; TRANSDIFFERENTIATION OF EPIDERMAL CELLS

FILE REFERENCE: P07 41494

CURRENT APPLICATION NUMBER: US/09/234,332A

CURRENT FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 16

SOPTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 5

LENGTH: 3138
CLASSIFICATION: 514
PRIOR APPLICATION UNMBER: FR 95/04558
PRICATION NUMBER: FR 95/04558
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR96/00560
FILING DATE: 12-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky Esq., Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: 29,699
REFERENCE/DOCKET NUMBER: 29,609-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 31; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dick
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: GLUCOSE-INDUCIBLE RECOMBINANT VIRAL TITLE OF INVENTION: VECTOR NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CHEN, Ruihuan
APPLICANT: DOIRON, Bruno
APPLICANT: KAHN, Axel
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 19426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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500 Arcola Road, Mailstop 3C43
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73.8%;
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Pred. No. 20;
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; MOLECULE TYPE:
US-08-775-428-1
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 Query Match 47.1%;
Best Local Similarity 75.0%;
Matches 30; Conservative
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Best Local Similarity
Matches 24; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sathe, Ganesh
APPLICANT: Fuetterer, Wendy
APPLICANT: Bergsma, Derk
APPLICANT: Bergsma, Derk
APPLICANT: Ellis, Catherine
TITLE OF INVENTION: cDNA CLONE HNFJD15 THAT ENCODES
TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1498 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: AT TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 1
FILING DATE: 09-JAN-:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
ZIP: 19406
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            %; Score 24; DB 3
%; Pred. No. 16;
0; Mismatches
Score 24; DB 2; Length 1498;
Pred. No. 25;
0; Mismatches 10; Indels
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US-09-016-434-1017/c
; Sequence 1017, Application US/09016434
; Patent No. 6500938
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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SEQ ID NO 60944
LENGTH: 601
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 60944, Application US/09949016 Patent No. 6812339
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Best Local :
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY Zeller, Karen J.
REGISTRATION NUMBER: 37,07
REFERENCE/DOCKET NUMBER: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                             STATE: C
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STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                         HEREWITH
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                                                                                                                                                                                           US/09/016,434
                     37,071
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Pred. No. 37;
0; Mismatches
     PA-0002 US
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LENGTH: 2777;
TYPE: DNA; ORGANISM: Infectious pancreatic necrosis virus US-09-282-147-39
                                                                                                                                                                                                                                                                                 RESULT 11
US-09-949-016-1956/c
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APPLICANT: YAO, Kun

APPLICANT: YAO, Kun

TITLE OF INVENTION: METHOD FOR GENERATING NON

TITLE OF INVENTION: FANCREATIC NECROSIS VIRUS

TITLE OF INVENTION: TRANSCRIPTS

FILE REFERENCE: 8288-9023

CURRENT APPLICATION NUMBER: US/09/282,147

CURRENT FILING DATE: 1999-03-31

EARLIER APPLICATION NUMBER: US/60/080,278

EARLIER APPLICATION NUMBER: PCT/US97/12955

EARLIER APPLICATION NUMBER: PCT/US97/12955

EARLIER APPLICATION DATE: 1998-03-31
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                                                                                                                           Sequence 1956, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Patent No. 6274147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (650) 845-410 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 659 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: CL. 930839
                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 45.9%;
Local Similarity 73.2%;
nes 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                         1077 AGGGGGCACTCCAGATGTTCCTGGTCTTCAGGTCCCAGTCT 1037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METHOD FOR GENERATING NONPATHOGENIC, INFECTIOUS PANCREATIC NECROSIS VIRUS (IPNV) FROM SYNTHETIC RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.9%;
73.2%;
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Pred. No. 38;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23.4; DB 3; Pred. No. 44; 0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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APPLICATION NUMBER: 60/231,498

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US-09-023-655-1294
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; ORGANISM: Human
US-09-949-016-1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1956
LENGTH: 3078
                                                       Matches
                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1294, Application US/09023655 Patent No. 6607879
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Best Local S
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APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                         IMMEDIATE SOURCE
LIBRARY: GENB
                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3174 PORTI
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                               NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304
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11 CGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 51
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                                                       Conservative
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                                                                   45.9%;
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73.2%;
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                                                                     Score 23.4;
Pred. No. 44;
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Pred. No. 4
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                                                       Mismatches
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                                                                                   DB 4; Length 3088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 3078;
                                                     11;
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                                                       Indels
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Sequence 49730, Application US/09949016

PAtent NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSITILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER: OF SEQ ID NOS: 207012
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 49730
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RESULT 15
US-09-949-016-49731/c
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/337,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/331,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                              Matches
                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                   LENGTH: 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 67.
                                                                                                                                                                                Local Similarity
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                                                                                 453
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                                                                                                                                                              31;
                                                                                                                    4 GGGCGCACGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAG 47
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                                                                                                                                                            Conservative
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                                                                                                                                                                              Score 23.2;
Pred. No. 44;
                                                                                                                                                              Mismatches
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OF DETECTION AND USES THEREOF
                                                                                                                                                                                               Length 601;
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Fatent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION WIMBER: US/09/949.016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/2317,768
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 66/231,498
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 66/231,498
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 66/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER: OF SEQ ID NOS: 207012
SOFTMARE: PASSEEQ for Windows Version 4.0
SEQ ID NO 49731
LENGTH: 601
TYPE: DNA
CORGANISM: Human
US-09-949-016-49731
Query Match
Best Local Similarity 70.5%; Score 23.2; DB 4; Length 601;
Best Local Similarity 70.5%; Pred N. 44;
Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY
4 GGGCGACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCAG 47
US GAGCAACCGTGCCTTCCCTTGATTCTTGGACTCCAG 47
US GAGCAACCGTGCCTTCCCTTGATTCTTGGACTCCAG 409
Search completed: September 1, 2005, 07:07:03
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                     seq length: 0 seq length: 2000000000
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270
1 catgggcgcacggg
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1: geneseqn1980s:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
geneseqn2003cs:*
geneseqn2003ds:*
geneseqn2004as:*
geneseqn2004bs:*
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geneseqn2003bs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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51	51	51	51	51	60.8	60.8	60.8	76.4	76.4	76.4	76.4	76.4	76.4	219	219.4	219.4	270	270	Score		
18.9	18.9	18.9	18.9	18.9	22.5	22.5	22.5	28.3	28.3	28.3	28.3	28.3	28.3	81.1	81.3	81.3	100.0	100.0	Match	*	
13011	372	321	194	51	6134	6128	6128	5001	1500	1500	1500	1500	1500	219	372	321	423	270	Match Length		
10	σ	σ	N	σ	4.	10	δ	4	12	10	10	10	σ	σ	Q	σ	σ	0	Bd		
ABT42448	ABX15375	ABX15374	AAT43002	ABX15371	AAH57489	ABV75371	ABN95896	AAH22429	ADP72689	ABT41911	ADB52710	ADB58201	ABK63701	ABX15372	ABX15375	ABX15374	ABX15376	ABX15373	ID		SUMMARIES
ABC96631 CDNA enco Abc42448 Toxicity		Abx15374 Rat insul		Abx15371 Rat gluco	Aah57489 Human liv	Abv75371 Human IGF	Abn95896 Gene #239	Aah22429 Rat insul	_	Abt41911 Toxicity	Adb52710 Primary r		Abk63701 Rat seque	Abx15372 Rat insul	Rat		٠.	Abx15373 Rat insul	Description		

The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene

Claim 9; Page 13-14; 37pp; English.

New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin liver cells.

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WPI; 2002-674190/72.

45	44	43						c 37				c 33	32		c 30	29	28			c 25			22	21
31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	32	. 32.2	32.4	33.2	33.4	33.4	35	37.8	37.8	37.8	48	48	51
11.7								11.7				11.9										17.8	17.8	18.9
1555	1555	1555	1550	1513	1348	1344	1288	1129	1125	927	548	76180	4447	1048	650	2667	1806	3895	7061	7061	7061	51	48	13011
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ADB32644	AAS39684	AAK90027	AAF94450	ADI16493	ABX71176	ABL57731	ADC87210	AAD33646	AAF94440	ABL57730	ADQ51481	ABD33385	AAT14078	AAS69850	ABZ52705	ADM03554	ABQ75795	ABN87725	AAS61189	ABL70248	ABL32997	ABX15380	ABX15379	ADP72914
Adb32644 Human nov	Aas39684 Genomic s	Aak90027 Human dig	Aaf94450 Human hyd	Adi16493 Human NOV	Abx71176 Novel hum	Abl57731 Human sbg	Adc87210 Human GPC	Aad33646 Human TRI	Aaf94440 Human hyd	Abl57730 Human sbg	Adq51481 Novel can	Abd33385 Human can	Aat14078 Pig dihyd	Aas69850 DNA encod	Abz52705 Aspergill	Adm03554 Human cDN	Abq75795 Human MDD		Aas61189 Human gen	Abl70248 Chemicall	Abl32997 Human imm	Abx15380 Rat liver	Abx15379 Rat liver	Adp72914 Renal tox

ALIGNMENTS

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RESULT 1
ABX15373
ID ABX1
Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; callular protein degradation; antidiabetic; intracellular hormone receptor; insulin regulator construct; anabolic.
                                                                                                                                                                                   11-OCT-2000; 2000US-0239113P.
                                                                                                                                                                                                          10-OCT-2001; 2001US-00972916.
                                                                                                                                                                                                                                    08-AUG-2002.
                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                            Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                       Rat insulin regulator construct DNA #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABX15373;
                                                                                                                                                                                                                                                           US2002107198-A1
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RESULT 2
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Best Local Sim:
Matches 270;
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11-OCT-2000; 2000US-0239113P
                                                                                                                                                                                                     glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic;
                                                                                                                                                                                                                                      Glucose response element; GJRE; liver pyruvate kinase; LPK; ds; IGFBP-insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulininsulin-like growth factor inding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat;
                            10-OCT-2001; 2001US-00972916.
                                                                  08-AUG-2002
                                                                                                                                                     Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                  ABX15376
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                                                                                                                                                                                       intracellular hormone
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                                                                                                                                                                                       receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270
                                                                                                                                                                                       regulator construct; anabolic
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RESULT 3
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AC ABX1
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Best Local Sim:
Matches 270;
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Pred. No. 3.8e-77
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Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose;

Rat insulin regulator construct

DNA #2

17-APR-2003

(first entry

ABX15374 standard; DNA;

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Best Local (
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281
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                                                                                                                                                                                                                                     50 TATCACAAACAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAAT 109
                                                                                                                                                                                                                     TGTCACAAGCAAAACTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAAT
                                                                                                       GTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGC
                                                                                                                                           CCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC 270
                                                                    GTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGC
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                     A; 111 C;
                                                                                                                                                                                                                                                                                                               81.3%;
99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                               Score 219.4; DB 6
Pred. No. 8.7e-61;
                                                                                                                                                                                                                                                                                                                                                                     84 G;
                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                     49 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                DB 6;
                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                  321;
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RESULT 4 ABX15375

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                                                                                                                                                                                               CC glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene
CC promoter and an insulin-sensitive element (ISE) of an insulin-like growth
CC factor binding protein-1 (IGFB-1) basal promoter. The construct is used
CC to treat or prevent diabetic complications, to regulate insulin
CC production, to modulate hyperglycaemia (without severe hypoglycaemia), to
CC increase fat catabolism and to retard protein catabolism. The construct
CC provides stimulation of insulin expression by glucose (but not other
CC carbohydrates) and glucocorticoids and inhibition by glucagen so that a
CC combination of these effects can maintain nearly euglycaemic conditions
CC in diabetics during short-term fasting, large carbohydrate loads or when
CC fed ad libitum and prevent pathological ketogenesis and ketoacidosis,
CC thus inhibiting the long-term complications of diabetes. The proporties
CC differentiated hepatoma lines and insulin expression in these cells may
CC have effects additional to those provided by secreted insulin, e.g.
CC inhibition of cellular protein degradation, and inhibition, or
CC stimulation of other intracellular hormone receptors. This sequence
CC represents a rat insulin regulator construct of the invention
                                                                                                                      Query Match
Best Local Similarity
Matches 220; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1 insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulir insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatoma; cellular protein degradation; antidiabetic;
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insuliver cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an insulin regulator construct comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 14; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-674190/72.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABX15375 standard; DNA; 372 BP
                                                                                     50
                                                                                                                                                                                               372
TATCACAAAGCAAAACAAACTTATTTTGAACACGGGGGATCCTAGCACGCTGCCCTGACAAT 109
                                                  TGTCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAAT
                                                                                                                    81.3%;
nilarity 99.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulator construct DNA
                                                                                                                                                                                               BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hormone receptor; insulin regulator construct; anabolic
                                                                                                                                                                                             87 A; 128 C; 102 G;
                                                                                                                    Score 219.4; DB 6
Pred. No. 9.2e-61;
0; Mismatches 1
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                                                                                                                                                                                               55 T;
                                                                                                                                                     DB 6;
                                                                                                                                                                                             0 U; 0 Other;
                                                                                                                        1;
                                                                                                                                                      Length
                                                                                                                                                          372;
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                                                                                                                        Gaps
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RESULT 5
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                                                              in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, e.g. inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat insulin-sensitive element of the invention
                                                                                                                                                                                                                                                                                                                                                                                   to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucocorticoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growth factor binding protein-1 (IGFBP-1) basal promoter. The construct is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insuliinsulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Page 13; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-OCT-2000; 2000US-0239113P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2002107198-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat insulin-sensitive element (ISE) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABX15372;
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intracellular hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCCACTGCCCGCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGC 331
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insulin;
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Query Match Best Local Similarity

100.0%; 81.1%;

Score 219; Pred. No. G;

Length 219;

Sequence 219

B₽;

57

A; 77 C;

48

37 T; 0 U; 0 Other; DB 6; le-60;

The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the global changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the hepatotoxicity of a compound, comprising detecting the level of expression in a tissue or cell sample exposed to the compound of two comore genes listed in the specification, where differential expression the genes is indicative of at least one toxic effect or progression. T

effect

the

progression. The

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RESULT 6
ABK63701
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XX ABK6
XX ABK6
XX ABK6
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                                                                                                                                                                                                                                                                                                                           Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-2000;
02-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat; ss; hepatotoxin; differential expression
                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-241625/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mendrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUN-2001;
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22-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat sequence differentially expressed in response to a hepatotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUN-2002
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                                                                                                                                                                                                                                                                                                       or to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENE
                                                                                                                                                                                                                                                         SEQ ID NO 1608; 239pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; cDNA; 1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC
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                                                                                                                                                                                                                                                                                                          cells.
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2000US-0244880P.

2001US-0290029P.

2001US-0290645P.

2001US-0292336P.

2001US-0292336P.

2001US-0297457P.

2001US-0297457P.

2001US-029884P.

2001US-0303459P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed sequence tag; EST; drug screening on; centrilobular necrosis; steatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171
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RESULT 7
ADB58201
ID ADB5
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Best Local S
Matches 77
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15-MAR-2002; 2002US-0364045P
15-MAR-2002; 2002US-036405SP
30-DEC-2002; 2002US-0436643F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toxicity-related gene, SEQ ID 3227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB58201 standard; DNA; 1500
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                                                                   markers in liver tissues c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JAN-2003; 2003WO-US003194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Toxic; toxin; gene expression profile; hepatotoxicity; liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-DEC-2003 (first entry)
the compound
                                 comprises preparing
                                                                                                                                                                                                                                                   Mendrick D,
                                                                                                                                                                                                                                                                                                                              (GENE-) GENE LOGIC INC.
                                                                                                                                                                                2003-689530/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   screening; toxicity assay; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACTTCCGCTACTATCTA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACTICCGCTACTAGCTA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
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                                                                                                                                                                                                                                                       Porter M,
                                 gene
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98.7%;
                                                                                                                                                                                                                                                       Johnson
                             t of a compound, useful in identifying toxicity or cells for drug screening and toxicity assays, expression profile of tissue or cells exposed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 3.
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                                                                                                                                                                                                                                                   В,
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                                                                                                                                                                                                                                                   Castle A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC of a tissue or cell sample exposed to the compound, and comparing the CC of a tissue or cell sample exposed to the compound, and comparing the CC gene expression profile to a database comprising SEQ ID 1-4925, where CC differential expression of the gene indicates at least one toxic effect. The method is useful for predicting at least one toxic effect. CC compound, identifying an agent that modulates the onset or CC compound, identifying an agent that modulates the onset or CC progression of a toxic response, predicting the cellular pathways that a CC compound modulates in a cell, and identifying an agent that modulates at CC compound modulates in a cell, and identifying an agent that modulate at the conset or CC present invention using a database of genes having liver toxin-induced CC differential expression, are useful in identifying toxicity markers in CC liver tissues or cells for drug screening and toxicity assays. Note: The sequence data for this patent did not form part of the printed consecution, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
              13-MAR-2002;
16-APR-2002;
10-APR-2002;
10-APR-2002;
11-APR-2002;
11-APR-2002;
11-APR-2002;
11-APR-2002;
11-APR-2002;
19-APR-2002;
22-APR-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                        toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                               04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                               Primary rat hepatocyte toxicity modelling related gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB52710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 3227; 1156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; DNA; 1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC 67
2002US-0363534P.
2002US-0370134P.
2002US-0371135P.
2002US-0371150P.
2002US-0371413P.
2002US-0373601P.
2002US-0373602P.
2002US-0378370P.
2002US-0378379P.
2002US-0378652P.
2002US-0378653P.
2002US-0394230P.
2002US-0394230P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to a method for predicting a toxic effect
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                2002US-0353171P.
                                                                                                                                                                                                                                            2003WO-US003482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336 A; 408 C; 380 G; 376 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
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98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 76.4; DI Pred. No. 3.4e 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1500,
                                                                                                                                                                                                                                                                                                                                                                                      diagnostic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO:3252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT 19
ABT41911
ID ABT4
XX ABT4
XX ABT4
XX Toxi
XX Toxi
XX Toxi
XX Toxi
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Best Local S
Matches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
               22-MAY 2001; 2001US-0292335P.
13-JUN-2001; 2001US-0297539.
13-JUN-2001; 2001US-029825P.
10-JUN-2001; 2001US-0303807P.
                                                                                                  22-MAY-2002;
                                                                                                                                 28-NOV-2002
                                                                                                                                                                WO200295000-A2
                                                                                                                                                                                                                                                Toxic effect; gene expression profile; renal toxicity; toxicity
                                                                                                                                                                                                                                                                                                                    26-JUN-2003
                                                                                                                                                                                                                                                                                                                                                    ABT41911;
                                                                                                                                                                                                                                                                                                                                                                                    ABT41911 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1500 BP; 336 A; 408 C; 380 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
 10-JUL-2001;
                                                                                                                                                                                                                                                                                 Toxicity modelling related rat gene SEQ ID No 1613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 44; SEQ ID NO 3252; 874pp; English
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Elashoff M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-SEP-2002; 2002US-0407688P.
28-JAN-2003; 2003US-0442900P.
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                                                                                                                                                                                                norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACTTCCGCTACTAGCTA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACTTCCGCTACTATCTA 85
                                                                                                                                                                                                                                grug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                (first
                                                                                                  2002WO-US016173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porter M, Johnson K,
                                                                                                                                                                                                                               screening; toxicity assay; rat; ds.
                                                                                                                                                                                                                                                                                                                                                                                    DNA; 1500 BP
                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.3%;
98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 76.4; DB 10;
Pred. No. 3.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Higgs B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Castle A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1500;
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RESULT 10
ADP72689
ID ADP72
XX
AC ADP72
XX
AC ADP72
XX
XX
XX
AC ADP72
XX
XX
XX
AC ADP72
XX
XX

ADP72689

standard; DNA; 1500

ВP

67

Renal toxin progression gene 26-AUG-2004 (first entry)

marker #1278

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                                                                                                                                                                                                                                                                                                                                           REFERENCE REFERE
                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel method of predicting at least one toxic CC effect of a compound. The method comprises a gene expression profile of a CC tissue or cell sample exposed to the compound, and comparing the gene CC expression profile to a database comprising at least part of the data or information given in the specification. The methods are useful for CC predicting at least one toxic effect of a compound, predicting the renal CC confictive of a compound, or identifying toxicity markers in tissues or CC cells exposed to known renal toxin. The genes are useful as toxicity CC markers in drug screening and toxicity assays, in monitoring disease or CC physiological states, or disease progression. This polynucleotide crepresents a rat DNA sequence relating to the toxic effect database CC described in the specification. NOTE: The sequence data for this patent CC calls exposed to free printed specification, but was obtained in CC electronic format directly from the World Intellectual Property
                                                                                                                                                                                                                            Matches
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Best Local
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28-AUG-2001;
27-SEP-2001;
27-OCT-2001;
01-NOV-2001;
01-NOV-2001;
06-DEC-2001;
19-DEC-2001;
19-DEC-2001;
21-FEB-2002;
21-FEB-2002;
21-FEB-2002;
08-APR-2002;
08-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Predicting at least one toxic effect modeling, comprises preparing a gene cell sample exposed to the compound,
                                                                                                                                                                                                                                                                                                                                     Sequence 1500
                                                                                                                                                                                                                                                                                                                                                                                          Organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page; 446pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       profile to a database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-148464/14.
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                                                                                                                                                                    188
                                                    248 CACTTCCGCTACTAGCTA
68
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                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                            CACTTCCGCTACTATCTA
                                                                                                            CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
                                                                                                                                                                                                                            Conservative
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2001US-0315047P

2001US-032492BP

2001US-0330462P

2001US-0330867P

2001US-0331805P

2001US-0336144P

2001US-0346873P

2002US-0357843P

2002US-0357843P

2002US-0357844P

2002US-0357844P

2002US-0364134P

2002US-0370144P

2002US-0370144P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOGIC
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2002US-0372794P.
2002US-0371679P.
                                                                                                                                                                                                                                                                                                                                           B₽;
                                                                                                                                                                                                                                                                                                                                        336 A; 408 C; 380 G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INC.
                                                                                                                                                                                                                                                   28.3%;
98.7%;
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85
                                                    265
                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                      Score 76.4; DB 10 Pred. No. 3.4e-14;
                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Higgs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of a compound, useful for toxicity expression profile of a tissue or and comparing the gene expression
                                                                                                                                                                                                                                                                             DB 10;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agent will induce various specific kidney pathologies, such as nephritis, kidney necrosis, glomerular and tubular injury, or focal segmental glomerulosclerosis. The methods are useful for determining the similarity of a toxic response to one or more individual compounds and for predicting or elucidating the potential cellular pathways influenced, induced or modulated by the compound or test agent. The kit is useful for predicting or modelling the toxic response of a test compound, for monitoring the progression of renal disease states, for identifying genes that show promise as new drug targets and for screening known and newly designed drugs. This sequence corresponds to a gene marker used in the method of the invention. (Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1500 BP; 336 A; 408 C; 380 G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         effect (toxicity progression). The method is useful for predicting (the progression of) at least one toxic effect of a compound. The genes are useful as toxicity markers in drug screening and toxicity assays. The methods are useful for predicting the likelihood that a compound or test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of predicting (the progression of) a toxic effect of a compound by preparing a gene expression profile of a kidney tissue or cell sample exposed to the compound and comparing the gene expression profile to a database, or detecting the level of gene(s expression in a tissue or cell sample exposed to the compound, where differential gene expression compared to a control indicates a toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Predicting (the progression of) a toxic effect of a compound, for monitoring the progression of renal disease states, comprises preparing a gene expression profile of a kidney tissue or cell sample exposed to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ds; toxic effect; gene expression profile; kidney tissue; differential gene expression; toxicity progression; toxicity drug screening; toxicity assay; kidney pathology; nephritis; kidney necrosis; glomerular injury; tubular injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-460771/43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; SEQ ID NO 1278; 266pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      focal segmental glomerulosclerosis.
                                                                         248
8
                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                     CACTTCCGCTACTAGCTA 265
                                                                                                                                                                                                                         CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCCAGAGAGCTGTGACCAC
                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                              28.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnson KR, Castle A,
85
                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                              Score 76.4; DB 12;
Pred. No. 3.4e-14;
                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                 Length 1500;
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                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                     247
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RESULT 11 AAH22429 ID AAH22 XX

AAH22429 standard;

DNA; 5001

ВP

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RESULT 12 ABN95896

standard; DNA; 6128

ВP

ABN95896 st; ABN95896; 13-AUG-2002

(first entry)

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                                                                                                                                                                                                  The present invention describes a method of screening a test agent for chepatotoxicity. The method comprises: (a) providing a test cell population comprising a cell capable of expressing one or more nucleic acid sequences selected from the group consisting of RISKWARKER 1-8 and INJURYWARKER 1-10; (b) contacting the test cell population with a test agent; (c) measuring expression of one or more of the nucleic acid sequences in the test cell population; (d) comparing the expression of the nucleic acid sequence in the test cell population to the expression of the nucleic acid sequence in an reference cell population comprising at least one cell whose exposure status to a hepatotoxic agent in known; and (e) identifying a difference in expression levels of the RISKWARKER or INJURYMARKER sequences, if present in expression levels of the RISKWARKER certain cell population. The method is useful for identifying a hepatotoxic agent. The present sequence is given in the exemplification of the patotoxic agent. The present sequence is given in the exemplification
                                                                                                                                Query Match
Best Local S
Matches 77
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18-FEB-2000;
20-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening hepatotoxic agent comprises contacting test cell population expressing RISKMARKER or INJURYMARKER with agent, comparing expression with reference population and identifying difference in expression
                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 22-24; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gould-Rothberg BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-355948/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identification; toxic; hepatotoxic; differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insulin-like growth factor binding protein nucleotide sequence
                                                                                    248 CACTTCCGCTACTAGCTA
61
                                                                                                                                 77;
                                                                ,_
                                                                                                                                                                                                                                  present
                                                                                                                                                 Similarity
                                                                                                                                                                                                  5001 BP; 1225 A; 1204 C; 1261 G; 1311 T; 0 U; 0 Other;
                                                                CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
                                                                                                                                 Conservative
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2000US-0183531P.
2000US-00717321.
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                                                                                                                                                                                                                                    invention
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                                                                                                                                               28.3%;
98.7%;
 78
                               265
                                                                                                                                 0;
                                                                                                                                                 Score 76.4; DB 4;
Pred. No. 5.3e-14;
                                                                                                                                 Mismatches
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                                                                                                                                                                 DB 4;
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                                                                                                                                                               Length 5001;
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                                                                                                                                 Gaps
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Gene

#2394 used

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diagnose liver cancer.

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RESULT 13
ABV75371
ID ABV75
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Best Local :
              ABV75371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatcocllular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                            ABV75371 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6128 BP; 1504 A; 1497 C; 1504 G; 1623 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing and detecting the progression carcinoma or metastatic liver tumor in a level of expression of two or more genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 2394; 298pp; English.
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metastatic liver tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumour in a patient, and differentiating metastatic liver cancer from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                    53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           iver cancer; ds; hepatocellular carcinoma; hepatotropic;
tic liver tumour; cytostatic; expression profile; disease state;
progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                       CAGCATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGC-ACACGG
                                                                                                                                                                                                                                                                                        TAACCC----
                                                                                                                                                                                                                                                                                                                      CACTAGCAAAACAAACTTATTTTGAACACTCAGCTCCTAGCGTGCGGCGCTGCCAATCAT
                                                                                                                                                                                                                                                                                                                                       CACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCAT
                                                                                                                                                        CCATCTGCCCAGAGAGCTGTGACCACCACTTC
                                                                                                                                                                                         GAGCATCGGCCACCGCCATCC
                                                                                                                                                                                                                                                     TAACCTCCTGGTGCAAGTGGCGCGCGCTGTGCCCCTTTATAAGGTGCGCGCTGTGTCCAGC
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                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                  22.5%;
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                                            6128
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                                            ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                  Score 60.8;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                         CATCCAGCGAGCATCTGCCGCCGCGCCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                    .5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of liver cancer, hepatocellular patient, involves detecting the in a liver tissue sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vockley
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                                                                                                                                                                                                                                                                                                                                                                                                                   DB
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                                                                                                                                                                                                                                                                                                                                                                                                                 6;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 6128;
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a liver cancer in a patient. The method involves detecting in a biological sample obtained from the patient aberrant expression of a gene encoding an insulin-like growth factor binding protein (IGRBP). The method is useful for detecting the presence or diagnosing the risk of a liver cancer or for screening agents in a patient. The agent is useful for the manufacture of a medicament for treating and/or preventing liver cancer. The present sequence represents a human IGFBP-1 polypeptide encoding genomic DNA (GenBank Accession No. M74587)
Sequence 6128 BP; 1504 A; 1497 C;
                                                                                                 The invention relates to detecting the presence or diagnosing a liver cancer in a patient. The method involves detecting in
                                                                                                                                Example; Page 104-108; 142pp; English.
                                                                                                                                                                  Detecting the presence or diagnosing the risk of a liver cancer in patient comprises detecting aberrant expression of a gene encoding
                                                                                                                                                                                                                                                                       (NACA-)
                                                                                                                                                                                                                                                                                                     03-MAY-2001; 2001US-0288441P
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                                                                                                                                                                                                                                                           (ARGA/)
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                                                                                                                                                                                                               2003-103522/09.
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                                                                                                                                                                                                                                                          SINGAPORE GEN HOSPITAL ARGAET V P.
                                                                                                                                                                                                                                                                                NAT CANCER CENT SINGAPORE PTE LTD
                                                                                                                                                                                                                                     Chow PKH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                growth factor binding protein; IGFBP; cytostatic; liver;
n; IGFBP-1; gene; ds.
                                                                                                                                                        growth
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2827. .4040
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4170. .5068
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5069. .5197
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2657. .2826
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762. .5200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "IGFBP-1"
/note= "insulin-like
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                                                                                                                                                      factor binding protein.
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1623 T; 0 U; 0 Other;
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                                                                                                             the risk of
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Query Match

22.5%;

Score 60.8;

В

10;

Length 6128;

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RESULT 14
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                AAH57161 to AAH57576 represent cell and tissue specific polynucleotide sequences (I). (I) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (I) and proteins (II) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids, mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (I) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a cancer, immunopathology or neuropathology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene associated with a cancer, immunopathology or neuropathology.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human liver cell specific cDNA sequence SEQ ID NO:329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH57489 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss; netabolic disease; developmental disease; cytostatic; immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; tissue specific; diagnosis; brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 246-248; 327pp;
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Best Local Similarity
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          The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPR) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growth factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucocorticoids and inhibition by glucagon so that a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP: insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic; intracellular normone receptor; insulin regulator construct; anabolic.
                                                                                                                                                                                                                 New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insuliver cells.
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                                                                                                                                                                              7; Page 13; 37pp; English
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Pred. No. 6.5e-09
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insulin;
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can maintain

euglycaemic conditions

Search completed: September 1, 2005, 00:34:43 Job time : 288.304 secs Query Match 18.9%; Score 51; DB 6; Length 51; Best Local Similarity 100.0%; Pred. No. 1.7e-06; Matches 51; Conservative 0; Mismatches 0; Indels in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, e.g. inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat glucose response element of the invention Sequence 51 BP; 6 A; 18 C; 17 G; 10 T; 0 U; 0 Other; 0; Gaps 0;

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Adp72914 Renal tox Abx15380 Rat liver	m	Aat43002 Rat type	Aah57489 Human liv	Abv75371 Human IGF	Abn95896 Gene #239	Aah22429 Rat insul	Adp72689 Renal tox	Abt41911 Toxicity		Adb58201 Toxicity-	Abk63701 Rat seque	•	Abx15372 Rat insul	Abx15376 Rat insul	Abx15373 Rat insul		Abx15374 Rat insul	Description

The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene

Claim 9; Page 14; 37pp; English.

New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin in liver cells.

WPI; 2002-674190/72.

(THUL/) THULE P M.

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9.8	9.8	9.8	9.8	9.8	9.8	9.8	9.8	9.9	10.0	10.0	10.0	10.1	10.3	10.9			11.4			11.8		15.0	15.9	15.9
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Adi16493 Human NOV		Abl57731 Human sbg	Adc87210 Human GPC	Aad33646 Human TRI	Aaf94440 Human hyd	Human	Adq51481 Novel can	Acn45138 Human gen	Acn44410 Human gen			Abx04971 S. cinnam	Abz52705 Aspergill	Abn87725 Human pro	Ach34858 Human end		Abs70481 Human bon	Ada52441 Human cod	Aas61189 Human gen	Abl70248 Chemicall	Huma		Abx15373 Rat insul	Abx15371 Rat gluco

ALIGNMENTS

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Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; glucose; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; protein degradation; antidiabetic; hepatoma; cellular protein degradation; antidiabetic;
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                                                                                                                                                                                                                                                                                                                                                              intracellular hormone receptor; insulin regulator construct; anabolic
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XX Rat
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    08-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTCCGCTACTAGCTAGCCGC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCCGTGCTGCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAMACCCAGCGAGCATTGAACACTGCACACGCCCATCTGCCCAGAGAGCTGTGACCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an insulin-sensitive element (ISE) of an insulin-like growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; 111 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 321; DB 6; 100.0%; Pred. No. 4.4e-89;
                                                                                                                                                                                                                                                                                                                        cellular protein
                                                                                                                                                                                                                                                                               receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                                                                                                                                                                                                               insulin
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                                                                                                                                                                                                                                                                                                                    degradation;
                                                                                                                                                                                                                                                                               regulator construct; anabolic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            insulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGFBP-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an insulin regulator construct comprising a CC glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene CC promoter and an insulin-sensitive element (ISE) of an insulin-like growth CC factor binding protein-l (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin (CC production, to modulate hyperglycaemia (without severe hypoglycaemia), to cincrease fat catabolism and to retard protein catabolism. The construct CC provides stimulation of insulin expression by glucose (but not other CC carbohydrates) and glucocorticoids and inhibition by glucagon so that a CC combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when CC thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-conditions inhibition of cellular protein degradation, and inhibition, or construct of cellular protein degradation, and inhibition, or construct are at insulin regulator construct of the invention
                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
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                                                                                                                                                                                                                                                                                                                                                                                                         Local
352
                              301
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                                                                                                                                                                                                                                                                                                                                                                                        321;
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                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 BP; 87 A; 128 C; 102 G;
                  CTTCCGCTACTAGCTAGCCGC 321
                                                                                  TATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCGTGCTGCCGAG
                                                                                                                                                                                                                                                                                          TACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGG
CTTCCGCTACTAGCTAGCCGC 372
                                                               CAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCCAGAGAGCTGTGACCACCA
                                                                                                                            CCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGGCGAGACA
                                                                                                                                                          CCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACA
                                                                                                                                                                                             TATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCGTGCTGCCGAG
                                                                                                                                                                                                                                                          TACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGG
                                                                                                                                                                                                                                                                                                                                                                                        Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
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א.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 321;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                     4.7e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6;
                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 372;
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                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                               300
                                                                                                                                                                                                                             180
                                                               351
                                                                                                                              291
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17-APR-2003

(first entry)

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to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hyperglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucocorticoids and inhibition by glucagen so that a combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, e.g. inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1 insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulir insulin-like growth factor binding protein; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; dlabetes; fasting; ketogenesis; ketoacidosis; hepatowa; cellular protein degradation; antidiabetic; hepatowa; cellular protein degradation; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growth factor binding protein-1 (IGFBP-1) basal promoter. The construct is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 270 BP; 63 A; 95 C; 65 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-674190/72.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represents a rat insulin regulator construct of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (THUL/) THULE P M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2000; 2000US-0239113P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat insulin regulator construct DNA #1.
                                                                                        110
                 221
                                                                                                                                                       161
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                                                                                                                                                                                                                                                                                                                                                                   220;
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                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                           GTCCACTGCCCGACGACACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGC
                                                                                        TATCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAAT 109
                                                                                                                                                                                                                                                                 TGTCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAAT 160
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                            68.3%;
                                                                                                                                                                                                                                                                                                                                                     Score 219.4; 1
Pred. No. 1.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                            219.4; DB 6;
No. 1.1e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                                                            Gaps
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                     280
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Best Local Si Matches 220; Query Match

Similarity

68.3%;

Score 219.4; Pred. No. 1.3e-57; Mismatches

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Conservative

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                                                 The invention relates to an insulin regulator construct comprising a CC glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISB) of an insulin-like growth cCC product on insulin-sensitive element (ISB) of an insulin-like growth cCC production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other cC carbohydrates) and glucocorticoids and inhibition by glucagon so that a CC combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when cf ed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties confictions inhibition the sesentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may call the confiction of cellular protein degradation, and inhibition, or similation of their intracellular hormone receptors. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-
insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insuli-
insulin-like growth factor binding protein-1; hypolycaemia; glucose;
fat catabolism; protein catabolism; catabolism; catabolism; glucose;
glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis;
hepatocyte; hepatoma; callular protein degradation; antidiabetic;
intracellular hores.
 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page 14; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-674190/72.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat insulin regulator construct DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABX15376
                                     represents a rat insulin regulator construct of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (THUL/) THULE P M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 intracellular hormone receptor; insulin regulator construct; anabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281
   423
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   Other;
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The invention relates to an insulin regulator construct comprising a CC glucose response element (GIRE) of a liver pyruvate kinase (IPK) gene CC promoter and an insulin-sensitive element (ISE) of an insulin-like growth CC factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin CC production, to modulate hyperglycaemia (without severe hypoglycaemia), to cincrease fat carabolism and to retard protein catabolism. The construct CC provides stimulation of insulin expression by glucose (but not other CC carbohydrates) and glucocorticoids and inhibition by glucagon so that a CC combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when CC fed ad libitum and prevent pathological ketogenesis and ketoacidosis, the construct are essentially specific for hepatocytes and well-CC differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, e.g.
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                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                  New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-674190/72.
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                                                                                                                                                                                                                                                                                                      Page 13; 37pp; English
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic; intracellular hormone receptor; insulin regulator construct; anabolic.
                                                                                                                                                                                             New insulin regulator cassette, useful e.g. for treating provides specific, glucose-inducible transgenic expressic liver cells.
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Pred. No. 1.4e-57;
Pred. No. 1.4e-57;
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The invention relates to an insulin regulator construct comprising glucose response element (GIRE) of a liver pyruvate kinase (LPK) ge promoter and an insulin-sensitive element (ISE) of an insulin-like factor binding protein-1 (IGFBP-1) basal promoter. The construct is

growth s used

to treat or prevent diabetic

complications,

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RESULT 7
ABK63701
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Best Local (
                            Predicting (
effects by o
exposed to (
tissues or o
                                                                                                                                                                                                                                                                                   02-NOV-2000;
11-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                               07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat; ss; hepatotoxin; ex: differential expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat sequence differentially expressed in response to a hepatotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucocorticoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitium and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, or inhibition of cellular protein degradation, and inhibition, or estimulation of other intracellular hormone receptors. This sequence
                                                                                                                                                                                                                                                                                                                  31-JUL-2000; 2000US-0222040P
                                                                                                                                                                                                                                                                                                                                                30-JUL-2001; 2001WO-US023872
                                                                                                                                                                                                                                                                                                                                                                                                            WO200210453-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK63701;
                                                                                                                                                                                                          13-JUN-2001;
19-JUN-2001;
                                                                                                                                                                                                                                          06-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK63701 standard; cDNA; 1500
                                                                                                                                                                                                                                                                      15-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 423 BP; 81 A; 149 C; 116 G; 77
                                                                                                                                                                (GENE-)
                                                                                                                                                                                                                                                        22-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represents a rat insulin regulator construct of the invention
                                                                                                      2002-241625/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             μ
                                                                                                                                                              GENE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCCATGT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCCGTGCGCCCATGTACACTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGG
                                     toxic effects of compounds or the progression of these toxic determining the changes in gene expression in tissues or cells the toxin and comparing these to gene expression in unexposed
                                                                                                                                                                                         ; 2000US-0244880P.
; 2001US-0290029P.
; 2001US-0290645P.
; 2001US-0292336P.
; 2001US-0292336P.
; 2001US-0295798P.
; 2001US-0298884P.
; 2001US-0303459P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                Porter MW,
                                                                                                                                                              LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed sequence tag; EST; drug screening; on; centrilobular necrosis; steatosis.
                                                                                                                                Johnson KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 103; DB 6; 1
Pred. No. 1.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                Castle AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 423
                                                                                                                                Elashoff MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #1608
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Claim 1;

SEQ ID NO 1608; 239pp; English

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RESULT 8
ADB58201
ID XXX AC XXX AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC expression in a tissue or cell sample exposed to the compound of two or controlled the genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression. The compound also be used to identify an agent which modulates in a controlled can also be used to identify an agent which modulates in a coll. The methods utilise a set of at least two probes (on a solid support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer comprising at database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification, conducted in the specification. The method is useful for elucidating global changes in gene expression and for identifying toxicity markers in consicity markers in drug screening and toxicity assays. The genes and consicity markers in drug screening and toxicity assays. The genes and consider that has been exposed to a compound or agent. Hepatotoxicity is sample that has been exposed to a compound or agent. Hepatotoxicity is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 77
                           31-JAN-2002;
15-MAR-2002;
15-MAR-2002;
30-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the global changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the progression of a toxic effect, preferably the
                                                                                                                                                                                             31-JAN-2003;
                                                                                                                                                                                                                                                              07-AUG-2003
                                                                                                                                                                                                                                                                                                                            WO2003064624-A2
                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toxic; toxin; gene expression profile; hepatotoxicity; liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toxicity-related gene, SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADB58201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB58201 standard; DNA; 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1500 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence tag (EST) or cDNA derived from a gene which is differentially expressed in response to a hepatotoxic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hepatotoxicity of a compound,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACTTCCGCTACTAGCTA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACTICCGCTACTATCTA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
                           2002US-00060087.
2002US-0364045P.
2002US-0364055P.
2002US-0436643P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                             2003WO-US003194
                                                                                                                                                                                                                                                                                                                                                                                                                                                        toxicity assay; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               336 A; 408 C; 380 G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.8%;
98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID 3227
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Pred. No. 3.2e-13;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprising detecting the level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1500;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
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RESULT 9
ADB52710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method for predicting a toxic effect CC of a compound. The method comprises preparing a gene expression profile CC of a tissue or cell sample exposed to the compound, and comparing the CC gene expression profile to a database comprising SEQ ID 14925, where CC The method is useful for predicting at least one toxic effect. CT of a compound, predicting hepatotoxicity or the progression of a toxic effect of a compound, identifying an agent that modulates the onset or CC progression of a toxic response, predicting the cellular pathways that a CC compound modulates in a cell, and identifying an agent that modulates at CC least one activity of a protein. The method and compositions of the CC differential expression, are useful in identifying toxicity markers in CC liver tissues or cells for drug screening and toxicity assays. Note: The sequence data for this patent did not form part of the printed consecution, but was obtained in electronic format directly from WIPO are ferre when in the format of the printed consecutions.
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
 04-FEB-2002;
13-MAR-2002;
08-APR-2002;
10-APR-2002;
10-APR-2002;
                                                                                                                                                                                                     toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
                                                                                        04-FEB-2003;
                                                                                                                    14-AUG-2003
                                                                                                                                                 WO2003065993-A2
                                                                                                                                                                           Rattus norvegicus
                                                                                                                                                                                                                                                               Primary rat hepatocyte toxicity modelling related gene
                                                                                                                                                                                                                                                                                               04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                    ADB52710 standard; DNA; 1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mendrick D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                           299
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                                                                                                                                                                                                                                                                                                                                                                                                                               83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCCAGAGAGCTGTGACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                             CACTTCCGCTACTATCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                CACTTCCGCTACTAGCTA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 3227; 1156pp; English
; 2002US-0353171P.
; 2002US-0363534P.
; 2002US-0370248P.
; 2002US-0371134P.
; 2002US-0371135P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                       2003WO-US003482.
                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porter
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                                                                                                                                                                                                                                                                                               entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                             85
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Pred. No. 3.2e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
).2e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other;
                                                                                                                                                                                                                                  diagnostic marker;
                                                                                                                                                                                                                                                                  SEQ ID NO:3252.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298
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RESULT 10
ABT41911
ID ABT41
XX ABT41
XX ABT41
XX TOXIC
DT 26-JU
XX TOXIC
XX TOXIC
XX TOXIC
XX TOXIC
XX ABT41
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                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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11-APR-2002;
19-APR-2002;
19-APR-2002;
22-APR-2002;
08-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mendrick
Elashoff
                                           Toxic effect; gene expression profile; renal toxicity; database; drug screening; toxicity assay; rat; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
                                                                                                                       26-JUN-2003
                                                                                                                                                                                 ABT41911 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1500 BP; 336 A; 408 C; 380 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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                                                                                                                                                                                                                                                                              CACTTCCGCTACTAGCTA 316
                                                                                       modelling
                                                                                                                                                                                                                                                           CACTICCGCTACTATCTA 85
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2002US-0371413P.
2002US-0373602P.
2002US-0373602P.
2002US-0378370P.
2002US-0378652P.
2002US-0378653P.
2002US-0378653P.
2002US-0378653P.
2002US-0394253P.
2002US-0394253P.
2002US-0394253P.
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                                                                                         related
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98.7%;
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                                                                                       rat gene SEQ ID No 1613
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                                                                                                                                                                                 ВP
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Pred. No. 3.
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1.2e-13;
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                                                             toxicity marker;
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Rattus norvegicus

WO200295000-A2

2001US-0292335P 2002WO-US016173

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Best Local :
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10-JUL 2001; 2001US-0303808P.
10-JUL 2001; 2001US-03038108P.
10-JUL 2001; 2001US-0303810P.
28-AUG-2001; 2001US-0315047P.
27-SEP-2001; 2001US-0334928P.
22-CCT-2001; 2001US-0330867P.
01-NOV-2001; 2001US-0331805P.
21-NOV-2001; 2001US-0331805P.
21-PEB-2002; 2002US-0357844P.
15-MAR-2002; 2002US-0357844P.
08-APR-2002; 2002US-0370144P.
08-APR-2002; 2002US-0370144P.
                                                                                                                                                                                                                  information given in the specification. The methods are useful for predicting at least one toxic effect of a compound, predicting the progression of a toxic effect of a compound, predicting the renal toxicity of a compound, or identifying toxicity markers in tissues or cells exposed to known renal toxic. The genes are useful as toxicity markers in drug screening and toxicity assays, in monitoring disease or physiological states, or disease progression. This polymucleotide represents a rat DNA sequence relating to the toxic effect database described in the specification. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the World Intellectual Property
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13-JUN-2001;
19-JUN-2001;
                                                                                                                                                                            Sequence 1500 BP;
                                                                                                                                                                                                      Organization
                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel method of predicting at least one toxic effect of a compound. The method compurises a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising at least part of the data or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell sample exposed to profile to a database.
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                                                                                                                               Local
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                                                                        CACTICCGCTACTAGCTA 316
CACTTCCGCTACTATCTA 85
                                                         CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
                                                                                                                  Conservative
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2002US-0372794P
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98.7%;
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Pred. No. 3.2e
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239 CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC 298

Query Match Best Local S Matches 77

l Similarity 77; Conser

23.8%;

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Score 76.4; I Pred. No. 3.2e 0; Mismatches

3.2e-13;

BB 12;

Length 1500;

0 Other;

Indels

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Gaps

Sequence 1500

BP; 336 A; 408 C; 380 G; 376 T; 0 U;

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RESULT 11
ADP72689
ID ADP72
The invention relates to a method of predicting (the progression of) a CC toxic effect of a compound by preparing a gene expression profile of a CC kidney tissue or cell sample exposed to the compound and comparing the cC gene expression profile to a database, or detecting the level of gene (s) expression in a tissue or cell sample exposed to the compound, where CC differential gene expression compared to a control indicates a toxic ceffect (toxicity progression). The method is useful for predicting (the CC progression of) at least one toxic effect of a compound. The genes are CC useful as toxicity markers in drug screening and toxicity assays. The CC useful as toxicity markers in drug screening and toxicity assays. The CC differential induce various specific kidney pathologies, such as nephritis, compound in the second or test agent will induce various specific kidney pathologies, such as nephritis, compound necrosis, glomerular and tubular injury, or focal segmental CC glomerulosclerosis. The methods are useful for determining the similarity of a toxic response; glomerular and tubular injury, or focal segmental CC predicting or elucidating the potential cellular pathways influenced, CC induced or modelling the compound or test agent. The kit is useful for predicting the progression of renal disease states, for identifying genes that show promise as new drug targets and for screening known and newly designed drugs. This sequence corresponds to a gene marker used in the CC method of the invention. (Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences).
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Elashoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ds; toxic effect; gene expression profile; kidney tissue; differential gene expression; toxicity progression; toxicity drug screening; toxicity assay; kidney pathology; nephritis; kidney necrosis; glomerular injury; tubular injury;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (the progression of) a toxic effect of a compound, for
the progression of renal disease states, comprises preparing a
seion profile of a kidney tissue or cell sample exposed to the
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RESULT 12
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                                                                                                                                                                                                             population comprising a cell capable of expressing one or more nucleic acid sequences selected from the group consisting of RISKWARKER 1-8 and INJURYMARKER 1-10; (b) contacting the test cell population with a test agent; (c) measuring expression of one or more of the nucleic acid sequence in the test cell population; (d) comparing the expression of the nucleic acid sequence in the test cell population to the expression of the nucleic acid sequence in an reference cell population comprising at least one cell whose exposure status to a hepatotoxic agent in known; and (e) identifying a difference in expression levels of the RISKWARKER or INJURYMARKER sequences, if present, in the test cell population and reference cell population. The method is useful for identifying a hepatotoxic agent. The present sequence is given in the exemplification
                                                                                                                                                                     Sequence 5001 BP; 1225 A; 1204 C; 1261 G; 1311 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method of screening a test agent hepatotoxicity. The method comprises: (a) providing a test cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 22-24; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening hepatotoxic agent comprises contacting test cell population expressing RISKMARKER or INJURYMARKER with agent, comparing expression with reference population and identifying difference in expression
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20-NOV-2000;
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non-steroidal antiinflammatory drug; ds.
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                                                                CACTTCCGCTACTAGCTA 316
                                               CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCCAGAGAGCTGTGACCAC
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Conservative
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2000US-00717321.
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98.7%;
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RESULT 13
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Best Local Similarity
                                                                                                                                                                                                                                                                                     Sequence 6128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.
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                                                                       498
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 CCTGTGCCCTTTATAAGGTGCGCGCTGTGTCCAGCGAGCATCGGCCACCGCCATCC----
                              AGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGA 238
                                                                       ACACTCAGCTCCTAGCGTGCGGCGCTGCCAATCATTAACCTCCTGGTGCAAGTGGCGCGC
                                                                                                       ACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCC-----
                                                                                                                                          Alvares C,
                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                 19.9%;
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                                                                                                                                                                                                                  Score 63.8; DB 6;
Pred. No. 3.9e-09;
0; Mismatches 72;
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RESULT 14
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             Detecting the presence or diagnosing the risk of a liver cancer patient comprises detecting aberrant expression of a gene encodi
                                                                                                                         03-MAY-2002; 2002WO-AU000558
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                                                                                                                                                                                                                                                                                    exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABV75371;
                                                            Huynh TH,
                                                                          (NACA-) NAT CANCER CENT SINGAPORE PTE LTD.
(SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.
(ARGA/) ARGAET V P.
                                                                                                          03-MAY-2001; 2001US-0288441P
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                                                                                                                                                                                                                                                                                                                                                                                                              cancer; human;
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      insulin-like growth
                                                                                                                                                                                                                                                                                                           intron
                                                                                                                                                                                                                                                                                                                                                                                                                   Insulin-like growth factor binding protein; IGFBP; cytostatic; liver;
                                     2003-103522/09
DB; ABB82757.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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                                                            Chow PKH,

    - CATCCAGCGAGCATCTGCCGCCGCCGCCGCCCACCCCCCAGAGAGCACTGGCCA

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note= "insulin-like growth factor binding protein;
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      factor binding
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Best Local S
Matches 156
New cell and tissue specific polynucleotides useful for diagnosis prognosis or monitoring of treatments for disorders where the gene associated with a cancer, immunopathology or neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss; metabolic disease; developmental disease; cytostatic; immunomodulatory; neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
                                                                                                                                                                                                                                                                                                                   04-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; tissue specific; diagnosis; brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human liver cell specific cDNA sequence SEQ ID NO:329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               liver cancer or for screening agents in a patient. The agent is useful for the manufacture of a medicament for treating and/or preventing liver cancer. The present sequence represents a human IGFBP-1 polypeptide encoding genomic DNA (GenBank Accession No. M74587)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to detecting the presence or diagnosing the risk of a liver cancer in a patient. The method involves detecting in a biological sample obtained from the patient aberrant expression of a gene encoding an insulin-like growth factor binding protein (IGBBP). The method is useful for detecting the presence or diagnosing the risk of a method is useful for detecting the presence or diagnosing the risk of a method is useful for detecting the presence or diagnosing the risk of a method is useful for detecting the presence or diagnosing the risk of a method is useful for detecting the presence or diagnosing the risk of a method is useful for detecting the presence or diagnosing the risk of a method is useful for detecting the presence or diagnosing the risk of a method in the patients.
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                                                                                                                                                                                                                                                      (INCY-) INCYTE GENOMICS INC.
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                                                                                                                                                                                         Watson
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Pred. No. 3.9e.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1623 T; 0 U; 0 Other;
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CC AAH57161 to AAH57576 represent cell and tissue specific polynucleotide CC sequences (I). (I) can have cytostatic, immunomodulatory and CC neuroprotective activities, and can be used in gene therapy. (I) and CC proteins (II) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids, mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (I) in a sample indicates the differentiation of CC embryonic stem cells into a tissue selected from brain, heart, kidney, CC liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The CC developmental process, treatment, condition, disease or monitoring of treatments and for investigating a predisposition to a disorder where the CC gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the CC gene picture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.9
Best Local Similarity 63.2
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6134 BP; 1505 A; 1498 C; 1507 G; 1624 T; 0 U; 0 Other;
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670
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                                                                                                                           ----CATCCAGCGAGCATCTGCCGCCGCCGCCGCCGCCACCCTCCCAGAGAGCACTGGCCA
                                                                                                                                                                                       CACAAACCCAGCGAGCATTGAACACTGC-ACACGGCCATCTGCCCAGAGAGCTGTGACCA 297
                                                                                                                                                                                                                                                          CCTGTGCCCTTTATAAGGTGCGCGCGCTGTGTCCAGCGAGCATCGGCCACCGCCATCC----
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Pred. No. 3.9e-09;
0; Mismatches 72;
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Search completed: September 1, Job time: 342.384 secs 2005, 00:34:45

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Maximum Match 100%
Listing first 45 summaries
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1: geneseqn1980s:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

20	c 19	c 18			15	14	13	12	11	10	9	8	7	0 6	v	4	w	N	1	No.	Result	
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13.7	14.8	14.8	14.8	14.8	17.2	17.2	17.2	20.5	20.5	20.5	20.5	20.5	20.5	41.4	58.9	59.0	60.1	86.3	100.0	Match Length	Query	•
51	13011	13011	13011	194	6134	6128	6128	5001	1500	1500	1500	1500	1500	423	219	270	423	321	372			
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ABX15380	ADP72914	ABT42448	AAT96631	AAT43002	AAH57489	ABV75371	ABN95896	AAH22429	ADP72689	ABT41911	ADB52710	ADB58201	ABK63701	ABX15376	ABX15372	ABX15373	ABX15376	ABX15374	ABX15375	ij		SUMMARIES
Abx15380 Rat liver	Adp72914 Renal tox	Abt42448 Toxicity	Aat96631 cDNA enco	Aat43002 Rat type	Aah57489 Human liv	Abv75371 Human IGF	Abn95896 Gene #239	Aah22429 Rat insul		Abt41911 Toxicity	Adb52710 Primary r	Adb58201 Toxicity-	Abk63701 Rat seque		Rat	Rat	Rat		Abx15375 Rat insul	Description		

c 45						c 39		37	36		c 34			31	30			c 27			24		c 22	
34	34	34	34	34	34	35	35.6	35.8	35.8	36.2	36.6	36.6	36.8	37	37.4	37.6	37.6	37.8	37.8	37.8	38.6	48	51	51
9.1	9.1	9.1	9.1	9.1	9.1	9.4	9.6	9.6	9.6	9.7	9.8	9.8	9.9	9.9	10.1	10.1	10.1	10.2	10.2	10.2	10.4	12.9	13.7	13.7
10543	10543	10537	10537	10537	10537	3895	490	11009	11009	586	3054	1678	761	3896	12850	3191	1254	7061	7061	7061	44861	48	270	51
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AAK69583	AAS35770	ADJ07881	ADE46463	AAK69582	AAS35769	ABN87725	ACH34858	AAI70816	ABQ72907	ACH71991	ABS70481	ADA52441	ABL90266	ADQ64446	ADB36326	ACH87111	AAS77024	AAS61189	ABL70248	ABL32997	AAS20000	ABX15379	ABX15373	ABX15371
Aak69583 Human	Aas35770 Human car	Adj07881 Human car	Ade46463 Human car	Aak69582 Human imm	Aas35769 Human car	Abn87725 Human pro	Ach34858 Human end		Abq72907 Mouse lam	Ach71991 Human gen	Abs70481 Human bon	Ada52441 Human cod	Abl90266 Human pol	Adq64446 Novel hum	Adb36326 Human fac	Ach87111 Human gen		Aas61189 Human gen	Abl70248 Chemicall	Abl32997 Human imm	-	Rat	Rat	Abx15371 Rat gluco

ALIGNMENTS

ABX15375 standard; DNA; 372 BP.

17-APR-2003 ABX15375;

(first entry)

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RESULT 1
ABX15375
ID ABX15375
ID ABX1
XX ABX1
AC ABX1
XX Gluc
XW Insu
KW INTE
XX SYNT
XX INTE
OS Ratt
OS Ratt
OS SYNT
XX INTE
OS RATT

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                                                                                                                                                                                                                       New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin in liver cells.
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The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene

Claim 9; Page 14; 37pp; English.

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RESULT 2
ABX15374
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Best Local Similarity 100.
Matches 372; Conservative
                   Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-: insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulir insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; protein catabolism; protein degradation; antidiabetic; hepatoma; cellular protein degradation; antidiabetic;
                                                                                                                                                                                                                     Rat insulin
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     intracellular
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  hormone
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  insulin regulator construct; anabolic
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Synthetic Rattus norvegicus

RESULT 3

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Best Local Similarity
Matches 321; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucocorticoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growth factor binding protein-1 (IGFBP-1) basal promoter. The construct is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
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                       CTTCCGCTACTAGCTAGCCGC 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                             86.3%; Score 321; DB 6; Length 321; 100.0%; Pred. No. 2e-87;
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Matches 297
                                                                                                                                                                                                                                                                                         Sequence 423 BP; 81 A; 149 C; 116 G; 77 T; 0 U; 0 Other;
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The invention relates to an insulin regulator construct comprising a glucose response element (GIRS) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISB) of an insulin-like growth factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucocorticoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions
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insulin;
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Matches 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, e.g. inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat insulin regulator construct of the invention
                                                                  New insulin regulator cassette, useful e.g. for treating diabetes
                                                                                             WPI; 2002-674190/72.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Rat insulin-sensitive element (ISE) DNA.
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Claim 8;

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(THUL/) THULE P M.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; DNA; 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor; insulin regulator construct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No. 1.8e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other catbohydrates) and glucocorticoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, or inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence
   31-JUL-2000; 2000US-0222040P
02-NOV-2000; 2000US-0244880P
                                                                                              30-JUL-2001; 2001WO-US023872
                                                                                                                                                                                                                                                                                      Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                             differential
                                                                                                                                                                                                                                                                                                                                                                                        Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat sequence differentially expressed in response to a hepatotoxin #1608.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK63701 standard; cDNA; 1500 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 423 BP; 81 A; 149 C; 116 G; 77 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growth factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
                                                                                                                                                                                                                            WO200210453-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            represents a rat insulin regulator construct of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAGGAACCACGGGAGTGCCCCGTGCGCCCCATGT 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACACTGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                         expression; centrilobular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 154; DB 6; Pred. No. 1.2e-36;
                                                                                                                                                                                                                                                                                                                                                      necrosis; steatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51
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RESULT 8
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ADB58201 standard;

DNA;

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ADB58201

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350

CACTTCCGCTACTAGCTA 367 CACTICCGCTACTATCTA 85

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68

Matches

77;

Conservative

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CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCCAGAGAGCTGTGACCAC 67

Query Match Best Local Similarity

20.5%;

Score 76.4; DB (Pred. No. 7e-13; Mismatches

6 1:

Length 1500;

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Gaps

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CC cells. Also included are methods of predicting at least one toxic of a compound or progression of a toxic effect, preferably the CC hepatotoxicity of a compound, comprising detecting the level of CC hepatotoxicity of a compound, comprising detecting the level of CC expression in a tissue or cell sample exposed to the compound of two or CC more genes listed in the specification, where differential expression of CC expression also be used to identify an agent which modulates the toxic CC response and predict cellular pathways that a compound modulates in a CC cell. The methods utilise a set of at least two probes (on a solid CC support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer CC system comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a cet of genes comprising at least two genes listed in the specification, a computer CC supersision level in a tissue or cell of at least one gene CC isted in the specification. The method is useful for elucidating global CC changes in gene expression level in a tissue or cell of at least one gene CC isted in the specification. The method is useful for elucidating global CC toxicity markers in drug genes mand for identifying toxicity markers in CC tissues or cell exposed to a known toxin. The genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAY-2001;
15-MAY-2001;
22-MAY-2001;
06-JUN-2001;
                                           toxicity markers in drug screening and toxicity assays. The genes and gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or ce sample that has been exposed to a compound or agent. Hepatotoxicity is characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence tag (EST) or cDNA derived from a gene which is differentially expressed in response to a hepatotoxic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the global changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or
Sequence 1500 BP; 336 A; 408 C; 380 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUN-2001;
19-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1608; 239pp; English
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2001US-0290645P.
2001US-0292336P.
2001US-0295798P.
2001US-0297457P.
2001US-0297884P.
2001US-0303459P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Porter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnson KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Castle AL,
376 T; 0 U; 0 Other;
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method for predicting a toxic effect CC of a compound. The method comprises preparing a gene expression profile CC of a tissue or cell sample exposed to the compound, and comparing the CC gene expression profile to a database comprising SEQ ID 1-4925, where CC The method is useful for predicting at least one toxic effect. CC The method is useful for predicting at least one toxic effect of a CC compound, predicting hepatotoxicity or the progression of a toxic effect of a compound, identifying an agent that modulates the onset or CC progression of a toxic response, predicting the cellular pathways that a CC compound modulates in a cell, and identifying an agent that modulates at least one activity of a protein. The method and compositions of the CC compound modulates in a cell, and identifying an agent that modulates at least one activity of a protein. The method and compositions of the CC present invention using a database of genes having liver toxin-induced CC differential expression, are useful in identifying toxicity markers in CC liver tissues or cells for drug screening and toxicity assays. Note: The sequence data for this patent did not form part of the printed compositions of the printed compositions of the printed compositions are composed to the printed compositions are composed to the printed compositions are composed to the printed compositions of the printed compositions are composed to the compositions are composed to the composition are composed to the composition printed compositions are composed to the composition print
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    04-DEC-2003
                                          ADB52710;
                                                                               ADB52710 standard; DNA; 1500 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprises preparing the compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mendrick D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2002; 2002US-00060087.
15-MAR-2002; 2002US-0364045F.
15-MAR-2002; 2002US-0364055P.
30-DEC-2002; 2002US-0436643P.
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                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                              350
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1500
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        B₽;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                       76.4; DB 10;
No. 7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                   G; 376 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hepatotoxicity;
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22-APR-2002;
08-MAY-2002;
09-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         toxic effect; gene expression profile; hepatotoxicit toxicity marker; toxicity progression; drug screenin primary rat hepatocyte toxicity modelling; gene; ds
WPI; 2003-731472/69
                           Mendrick D,
Elashoff M;
                                                                                                                             09-JUL-2002;
                                                                                                                                                          09-MAY-2002;
                                                                                                                                                                                                                              19-APR-2002;
                                                                                                                                                                                                                                                           10-APR-2002;
11-APR-2002;
                                                                                                                                                                                                                                                                                                                      08-APR-2002;
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13-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus.
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                                                                       (GENE-)
                                                                     GENE
                                                                                                                                                                                   2002US-0371150P
2002US-0371413P
2002US-0373601P
2002US-0373602P
2002US-037379
2002US-0378370P
2002US-0378370P
2002US-0378370P
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2002US-0370248P.
2002US-0371134P.
2002US-0371135P.
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                                                                     LOGIC INC
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2002US-0407688P
                                                                                                                                              2002US-0394230P
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2002US-0378665P
                                        Porter M,
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                                          Johnson
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                                          Higgs
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                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     related gene
                                          Castle
                                          P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostic marker;
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Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox mean values.

Claim 44; SEQ ID NO 3252; 874pp; English

genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The toxicity modelling related gene sequence from the present invention rat hepatocyte

Sequence 1500 B₽; 336 A; 408 ç; 380 ç, 376 T; 0 U; 0 Other;

밁 S Matches Query Match Best Local : 290 æ . Similarity 77; Conserv CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC 20.5%; ilarity 98.7%; Conservative 0; Score 76.4; I Pred. No. 7e-1 0; Mismatches 4; DB 10; 7e-13; 1; Length ٥, Gaps 67

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10-JUL-2001; 2001US-0303807P

10-JUL-2001; 2001US-0303808P

10-JUL-2001; 2001US-0303810P

28-AUG-2001; 2001US-0330462P

29-SEP-2001; 2001US-0330462P

21-NOV-2001; 2001US-0330462P

21-NOV-2001; 2001US-03318057P

21-NOV-2001; 2001US-033180544P

19-DEC-2001; 2001US-03318073P

21-FEB-2002; 2002US-0357843P

21-FEB-2002; 2002US-0357844P

15-MAR-2002; 2002US-0357844P

16-APR-2002; 2002US-0357044P

08-APR-2002; 2002US-03770144P

08-APR-2002; 2002US-0370206P

08-APR-2002; 2002US-03770206P

08-APR-2002; 2002US-0377294P

21-APR-2002; 2002US-0377299P
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13-JUN-2001;
19-JUN-2001;
The invention relates to a novel method of predicting at least one toxic effect of a compound. The method comprises a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising at least part of the data or information given in the specification. The methods are useful for predicting at least one toxic effect of a compound, predicting the progression of a toxic effect of a compound, predicting the renal coxicity of a compound, or identifying toxicity markers in tissues or cells exposed to known renal toxin. The genes are useful as toxicity markers in drug screening and toxicity assays, in monitoring disease or physiological states, or disease progression. This polynucleotide
                                                                                                                                                                                                             Predicting at least one toxic effect of a compound, useful for toxicity modeling, comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression
                                                                                                                                                                                                                                                                                                      Mendrick
                                                                                                                                                                       Example 4; Page; 446pp; English.
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                                                                                                                                                                                                                                                                                                                                 (GENE-)
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screening; toxicity assay; rat; ds.
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                                                                                                                                                                                                                                                                                                      Johnson
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                                                                                                                                                                                                                                                                                                   Higgs
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                                                                                                                                                                                                                                                                                                    Castle
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of a

glomerular

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ADP7269
ID ADP72
XX ADP73
XX ADP73
XX ADP74
XX ADP76
XX ADP77
XX ADP76
XX ADP76
XX ADP77
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Best Local
                  The invention relates to a method of predicting (the progression of) a toxic effect of a compound by preparing a gene expression profile of a kidney tissue or cell sample exposed to the compound and comparing the gene expression profile to a database, or detecting the level of gene(s) expression in a tissue or cell sample exposed to the compound, where differential gene expression compared to a control indicates a toxic effect (toxicity progression). The method is useful for predicting (the progression of) at least one toxic effect of a compound. The genes are useful as toxicity markers in drug screening and toxicity assays. The methods are useful for predicting the likelihood that a compound or test agent will induce various specific kidney pathologies, such as nephritis, the progression of the progression of the progression of the state of the likelihood that a compound or test agent will induce various specific kidney pathologies, such as nephritis.
                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; SEQ ID NO 1278; 266pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Predicting (the progression of) a toxic effect of a compound, monitoring the progression of renal disease states, comprises gene expression profile of a kidney tissue or cell sample exports.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ds; toxic effect; gene expression profile; kidney tissue; differential gene expression; toxicity progression; toxicity drug screening; toxicity assay; kidney pathology; nephritis; kidney necrosis; glomerular injury; tubular injury;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-460771/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Elashoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mendrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-NOV-2002;
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The present invention describes a method of screening a test agent for hepatotoxicity. The method comprises: (a) providing a test cell population comprising a cell capable of expressing one or more nucleic acid sequences selected from the group consisting of RISKMARKER 1-8 and INJURYMARKER 1-10; (b) contacting the test cell population with a test agent; (c) measuring expression of one or more of the nucleic acid sequences in the test cell population; (d) comparing the expression of the nucleic acid sequence in the test cell population to the expression of
                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                       Screening hepatotoxic agent comprises contacting test cell population expressing RISKMARKER or INJURYMARKER with agent, comparing expression with reference population and identifying difference in expression
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tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN9303-ABN97455 in a tissue sample. The method of the invention has hepatocropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                   Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the nucleic acid sequence in an reference cell population comprising at least one cell whose exposure status to a hepatotoxic agent in known; and (e) identifying a difference in expression levels of the RISKMARKER sequences, if present, in the test cell population and reference cell population. The method is useful for identifying a hepatotoxic agent. The present sequence is given in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; diseas
                                                                                                                                                                                                     progression
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                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 2394; 298pp; English.
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RESULT 14
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WO200290580-A1
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Pred. No. 7.3e-09;
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RESULT 15
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Matches 156;
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          Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss; metabolic disease; developmental disease; cytostatic; immunomodulatory;
                                                                     Human liver cell specific cDNA sequence SEQ ID NO:329
                                                                                                                               AAH57489;
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(SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.
(ARGA/) ARGAET V P.
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neuroprotective;

gene therapy; cancer;

immunopathology; neuropathology

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC AAH57161 to AAH57576 represent cell and tissue specific polynucleotide CC sequences (I). (I) can have cytostatic, immunomodulatory and consequences (II) can have cytostatic, immunomodulatory and CC neuroprotective activities, and can be used in gene therapy. (I) and CC proteins (II) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids, cominetics, peptides, proteins, agonists, antagonists, antibodies or their CC fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (I) in a sample indicates the differentiation of CC embryonic stem cells into a tissue selected from brain, heart, kidney, CC liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The CC developmental process, treatment, condition, disease or disorder where the gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene profile can be used for disparse; immunopathology or neuropathology
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Best Local Similarity
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene

Claim 9; Page 14; 37pp; English.

New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin in liver cells.

WPI; 2002-674190/72.

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8.9	8.9	8.9	8.9	8.9	8.9	8.9	B.9	9.1	9.1	9.6	9.6	9.6	9.7	9.7	10.1	10.5	10.8	10.9	11.0	11.3	11.4	12.0	12.1	12.1
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ADJ30178	ABX59428	AAL36440	AAS61189	ABL70248	ABL32997	ABQ54073	ABQ54072	AAI70816	ABQ72907	ADH57071	ADH62916	ADD00956	ABQ54068	ABQ54069	ABX15376	AAS77024	ACH71991	ADB36326	ADQ64446	ABX15379	ACH87111	AAS20000	ABX15371	ABX15380
Adj30178 Human mus	Abx59428 cDNA enco	Aal36440 Human mus	Aas61189 Human gen	Abl70248 Chemicall		Abq54073 Oligonucl	Abq54072 Oligonucl		Abq72907 Mouse lam	Adh57071 Genomic h	Adh62916 Human Jag	Add00956 Human Jag	Abq54068 Oligonucl	Abq54069 Oligonucl	Abx15376 Rat insul	Aas77024 DNA encod	Ach71991 Human gen	Adb36326 Human fac	Adg64446 Novel hum	Abx15379 Rat liver	Ach87111 Human gen	Aas20000 DNA encod	Abx15371 Rat gluco	Abx15380 Rat liver

ALIGNMENTS

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Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-]; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic; intracellular hormone receptor; insulin regulator construct; anabolic.
                                                                                                                                                                                                                              08-AUG-2002.
                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                      Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                            Rat insulin regulator construct DNA #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                     17-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABX15376 standard; DNA; 423
                                                                                                                                                                              11-OCT-2000; 2000US-0239113P
                                                                                                                                                                                                     10-OCT-2001; 2001US-00972916.
                                                                                                                                                                                                                                                    US2002107198-A1
                                                                                                                                                      (THUL/) THULE P M.
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RESULT 2
ABX15373
ID ABX1
XX ABX1
AC ABX1
AC ABX1
XX ABX1
XX ABX1
XX ABX1
CF RAT
XX INSU
KW INSU
KW INSU
KW INSU
KW INSU
KW INSU
KW FAT
KW Gluc
KW Hepa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabblism and to retard protein catabblism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucocorticoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, e.g. thibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat insulin regulator construct of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 423; Conserv
Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulinsulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocrticoid; rat. glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic;
                                                                                                                                                                  Rat insulin
                                                                                                                                                                                                                17-APR-2003
                                                                                                                                                                                                                                                              ABX15373;
                                                                                                                                                                                                                                                                                                           ABX15373 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 423 BP; 81
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                                                                                                                                                                                                                                                                                                                                                                                                                         421
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                                                                                                                                                                regulator construct
                                                                                                                                                                                                                                                                                                                                                                                                                         423
                                                                                                                                                                                                              (first
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                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                              entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 423; DB 6; 1
100.0%; Pred. No. 6.5e-121;
                                                                                                                                                                                                                                                                                                           270
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                                                                                                                                                                DNA #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ٥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 423;
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                                                                                           insulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                   IGFBP-1;
                                               rat;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabblism and to retard protein catabblism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucocorticoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may have affects additional in these cells may
                                                                                                                                                                                                                                                                                                                                                                                                                                                       inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat insulin regulator construct of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like gro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           have effects additional to those provided by secreted insulin, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an insulin regulator construct comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 13-14; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-674190/72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intracellular hormone receptor; insulin regulator construct; anabolic
241
                                394
                                                                   181
                                                                                                                                         121
                                                                                                                                                                          274
                                                                                                                                                                                                                                                214
                                                                                                                                                                                                                                                                                                                   154
                                                                                                                                                                                                                                                                                                                                                   270;
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                     TGACCACCACTTCCGCTACTAGCTAGCCGC
                                                                                                                                                             CATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTATCACAAGCA
                                                                                                                                                                                                                                                                                                        CATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTATCACAAGCA 213
                                                                                                      GCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTG
                                                                                                                                         AAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCGT
                                                                                                                                                                                                                                            AAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                        270 BP; 63 A; 95 C; 65 G; 47 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specific,
                                                                   GCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTG
                                                                                                                                                                                                                                                                                                                                                      Conservative
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М.
                                                                                                                                                                                                                                                                                                                                                                   63.8%;
                                                                                                                                                                                                                                                                                                                                                 Score 270; DB 6; L; Pred. No. 1.6e-73;
270
                                423
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                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                   Gaps
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ABX15375

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                                                                                                                                                                                                                     The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene CC gromoter and an insulin-sensitive element (ISE) of an insulin-like growth CC factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin (CC increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other CC carbohydrates) and glucocorticoids and inhibition by glucagenia (combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fee ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-construct are essentially specific for hepatocytes and well-construct additional to those provided by secreted insulin, e.g. tinhibition of cellular protein degradation, and inhibition, or represents a rat insulin regulator construct of the invention
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                                                                                                                                             Query Match
Best Local S
Matches 297
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                                                                                                                                                                                                                     Sequence 372 BP; 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page 14; 37pp; English.
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Synthetic.
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                                                                                                                                                                Similarity
GCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGGGGCCAGAGTC
                                cccaereracareececaceeeecacreccereerrecreeacrereecececeerera 153
                                                                                                       ACTCTGGCCCCAGTGTACATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCC
                                                                     ACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGGG
                                                                                                                                               Conservative
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                                                                                                                                                                                                                 A; 128 C; 102 G;
                                                                                                                                                              52.9%;
76.2%;
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                                                                                                                                                              Score 223.6;
Pred. No. 4.3
                                                                                                                                             Mismatches
                                                                                                                                                                                                                 55 T; 0 U; 0 Other;
                                                                                                                                                           4.3e-59;
                                                                                                                                                                               DB 6;
                                                                                                                                             74;
                                                                                                                                             Indels
                                                                                                                                                                             Length
                                                                                                                                                                                 372;
                                                                                                                                             19;
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RESULT 4
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ID ABX1
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The invention relates to an insulin regulator construct comprising a glucose response element (GIRS) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISB) of an insulin-like growth factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucocorticoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions
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                                                                                                                                                                                                                                                                                                                                                                                      New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin liver cells.
                                                                                                                                                                                                                                                                                                                           Claim 9; Page 14; 37pp; English
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                                                                               New insulin regulator cassette, useful e.g. for treating diabetes provides specific, glucose-inducible transgenic expression of instituer cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC The invention relates to an insulin regulator construct comprising a CC glucose response element (GJRE) of a liver pyruvate kinase (LPK) gene CC promoter and an insulin-sensitive element (ISE) of an insulin-like growth CC factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin CC production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct CC provides stimulation of insulin expression by glucose (but not other CC carbohydrates) and glucocorticois and inhibition by glucagon so that a CC combination of these effects can maintain nearly euglycaemic conditions CC indiabetics during short-term fasting, large carbohydrate loads or when CC fed ad libitum and prevent pathological kerogenesis and ketoacidosis, CC thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-CC differentiated hepatoma lines and insulin expression in these cells may care effects additional to those provided by secreted insulin, e.g. cinibition of cellular protein degradation, and inhibition, or represents a rat insulin-sensitive element of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 219; Conserv
Rat insulin regulator construct DNA #3.
                                         17-APR-2003
                                                                                  ABX15375;
                                                                                                                         ABX15375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                      385
                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                  121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219
                                                                                                                           standard; DNA; 372
                                                                                                                                                                                                                               AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC 219
                                                                                                                                                                                                                                                       AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC
                                                                                                                                                                                                                                                                                                                  CCACTGCCGGCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
                                                                                                                                                                                                                                                                                                                                            CCACTGCCCGACGACACACACACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                  TCACAAGCAAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 57 A; 77 C; 48 G; 37 T; 0 U; 0 Other;
                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.8%; Score 219; DB 6; 1 100.0%; Pred. No. 9.5e-58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 219,
                                                                                                                                                                                                                                                                        423
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RESULT 6
ABX15375/c
ID ABX153
XX ABX153
XX ABX153
XX ABX153
XX GRUCOS
KW INSULI:
KW INSU Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carabohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic; 11-OCT-2000; 2000US-0239113P Synthetic Rattus norvegicus. 10-OCT-2001; 2001US-00972916. US2002107198-A1 intracellular hormone receptor; insulin regulator construct;

Claim

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Page 13;

37pp; English

(THUL/) THULE P M

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RESULT 7
ABX15374/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                      Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-: insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulir insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic; interpretation; cellular protein degradation; antidiabetic;
               US2002107198-A1
                                                                    Rattus norvegicus
                                                                                                                                                                                                                                                          Rat insulin regulator construct DNA #2.
                                                                                                                                                                                                                                                                                                   17-APR-2003
                                                                                                                                                                                                                                                                                                                                       ABX15374;
                                                                                                                                                                                                                                                                                                                                                                            ABX15374 standard; DNA; 321 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 372 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin liver cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thule PM
                                                                                                            intracellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTACATGGGCGCACGGGGCA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTACATGGGCG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                          hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.4%; Dr.
100.0%; Pr.
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; 128 C; 102 G; 55
                                                                                                          receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 154; DB 6;
Pred. No. 1.6e-37
                                                                                                        insulin regulator construct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                   IGFBP-1;
insulin;
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RESULT 8
ABK63 MBK6
XX ABK6
XX ABK6
XX ABK6
XX ABK6
XX ABK6
XX BAT
XX Rat
XX Rat
XX Rat
XX Rat
XX AST
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XX O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an insulin regulator construct comprising a CC glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene CC promoter and an insulin-sensitive element (ISE) of an insulin-like growth CC factor binding protein-l (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin CC production, to modulate hyperglycaemia (without severe hypoglycaemia), to cincrease fat catabolism and to retard protein catabolism. The construct CC provides stimulation of insulin expression by glucose (but not other CC combination of these effects can maintain nearly euglycaemic conditions combination of these effects can maintain nearly euglycaemic conditions combination of these effects can maintain nearly euglycaemic conditions cf ed ad libitum and prevent pathogogications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-cations inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-cations of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat insulin regulator construct of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 103;
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30-JUL-2001; 2001WO-US023872
                                                                       07-FEB-2002
                                                                                                                                       WO200210453-A2
                                                                                                                                                                                                       Rattus norvegicus
                                                                                                                                                                                                                                                                          Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening; differential expression; centrilobular necrosis; steatosis.
                                                                                                                                                                                                                                                                                                                                                                              Rat sequence differentially expressed in response to a hepatotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK63701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK63701 standard; cDNA; 1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-674190/72.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.3%; So llarity 100.0%; I Conservative 0;
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Pred. No. le-21;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              CC expression in a tissue or cell sample exposed to the compound of two or come genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression. The come method can also be used to identify an agent which modulates in a cell. The methods utilise a set of at least two probes (on a solid compound in the specification, where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification, a computer comprises or comprising at least two genes listed in the specification, a computer comprision at least two genes listed in the specification, a computer comprision at least two genes listed in the specification, and a user interface to view the information used to present information contings in gene expression level in a tissue or cell of at least one gene containing at least two genes listed in the specification continues or cell exposed to a known toxin. The genes may be used as contained to present information may be used as diagnostic markers for the contained to a compound or agent. Hepatotoxicity is contained that has been exposed to a compound or agent. Hepatotoxicity is contained to a compound or agent. Hepatotoxicity is generate is an expressed sequence to a compound of agent. The present forms are contained as a contained to a compound or agent. The present forms are contained to a compound or agent. The present forms are contained to a compound or agent. The present forms are contained to a compound or agent. The present forms are contained to a compound or agent. The present forms are contained to a compound or agent. The present forms are contained to a compound or agent.
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02-NOV-2000;
11-MAY-2001;
15-MAY-2001;
22-MAY-2001;
06-JUN-2001;
                                                                                                                                                                                                                                                                                                                       Sequence 1500 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of a compound or progression of a toxic effect, preferably hepatotoxicity of a compound, comprising detecting the leve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cells. Also included are methods of predicting at least one toxic effect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     global changes in gene expression in tissues or cells exposed to toxin and comparing these to gene expression in unexposed tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cell exposed to the toxin and comparing these to gene expression in unexposed tissues or cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mendrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    compounds or the
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                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
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                                                                                                                                                                                                                                                         Similarity
                                                                                        CACTTCCGCTACTAGCTA 418
                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                                                                     is an expressed sequence tag (EST) or cDNA derived
                                                                CACTTCCGCTACTATCTA 85
                                                                                                                                                 CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
                                                                                                                                                                                                                                                                                                                                                                 differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1608; 239pp; English.
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0; 2000US-0244880P.
1; 2001US-0290645P.
1; 2001US-029336P.
1; 2001US-0292336P.
1; 2001US-029479P.
1; 2001US-029484P.
1; 2001US-0303459P.
                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  relates to methods for predicting toxic effects of the progression of these toxic effects by determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               progression of these toxic
                                                                                                                                                                                                                                                                                                                     336 A; 408 C; 380 G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INC.
                                                                                                                                                                                                                                                     18.1%;
98.7%;
                                                                                                                                                                                                                                                                                                                                                               expressed
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                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                   Score 76.4; DB 6;
Pred. No. 3.1e-13;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                             in response to a hepatotoxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Castle AL,
                                                                                                                                                                                                                                                                         Length 1500;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elashoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the level of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissues or
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                                                                                                                                                                                                                                                                                                                                                             agent
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IJ

ADB58201 standard; DNA; 1500 BP

RESULT 10 ADB52710

ADB52710 standard; DNA; 1500

ВP

ADB58201

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                                                                                                                                                                                    CC of a compound. The method comprises preparing a gene expression profile CC of a tissue or cell sample exposed to the compound, and comparing the CC gene expression profile to a database comprising SEQ ID 1-4925, where CC differential expression of the gene indicates at least one toxic effect. The method is useful for predicting at least one toxic effect of a compound, predicting hepatotoxicity or the progression of a toxic effect of a compound, identifying an agent that modulates the onset or CC progression of a toxic response, predicting the cellular pathways that a CC compound modulates in a cell, and identifying an agent that modulates at CC compound modulates in a cell, and identifying an agent toxin-induced CC present invention using a database of genes having liver toxin-induced CC differential expression, are useful in identifying toxicity markers in CC liver tissues or cells for drug screening and toxicity assays. Note: The sequence data for this patent did not form part of the printed consecution, but was obtained in electronic format directly from WIPO
                                                                                                                       Matches
                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-2002;
15-MAR-2002;
15-MAR-2002;
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 3227; 1156pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-689530/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JAN-2003; 2003WO-US003194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a method for predicting a toxic effect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003064624-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toxic; toxin; gene expression profile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toxicity-related gene, SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB58201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENE-) GENE
                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  screening;
                                                                                   341 CACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC 400
 83
                                                                                                                       77;
                                                           œ
                                                                                                                                       Similarity
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                    CACTTCCGCTACTAGCTA 418
                                                                                                                                                                                    1500
CACTTCCGCTACTATCTA
                                                           CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCCAGAGAGCTGTGACCAC
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOGIC INC
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2002US-0364055P.
2002US-0436643P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                   BP; 336 A; 408 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  toxicity assay;
                                                                                                                                    18.1%;
98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IJ
 85
                                                                                                                       0;
                                                                                                                                      Score 76.4;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3227
                                                                                                                      Mismatches
                                                                                                                                                                                    380 G;
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                                                                                                                                                                                    376 T;
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                                                                                                                                       .1e-13;
                                                                                                                                                    DB 10;
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U;
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                                                                                                                       Indels
                                                                                                                                                    Length 1500;
                                                                                                                                                                                    0 Other;
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                                                                                                                       0,
                                                                                                                       Gaps
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10-APR-2002;
11-APR-2002;
19-APR-2002;
19-APR-2002;
20-APR-2002;
08-MAY-2002;
09-MAY-2002;
09-MAY-2002;
                                                                                                                                                                                                                                                                                            04-FEB-2002;
13-MAR-2002;
08-APR-2002;
10-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening;
                                                                                                                                                                                                                                                                               10-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primary rat hepatocyte toxicity modelling related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADB52710;
(GENE-) GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rat
                              2002US-0363534P
2002US-0370248P
2002US-0371135P
2002US-0371135P
2002US-0371150P
2002US-0371413P
2002US-0373601P
2002US-0373601P
2002US-0374139P
2002US-0374139P
2002US-037853P
2002US-0378652P
2002US-0378652P
2002US-0378652P
2002US-0378652P
2002US-0378652P
2002US-0378652P
2002US-0378665P
2002US-0394230P
2002US-0394230P
2002US-0394230P
2002US-0407688P
2003US-0442900P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hepatocyte toxicity modelling; gene; ds
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                                                                                                                                                                                                                                                                                                                                                                                         2003WO-US003482
COGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NO:3252.
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Mendrick Elashoff Determining if a compound induces a toxic effect on a tissue or cell, identifying hepatotoxic compounds, comprises comparing a gene express profile of a tissue or cell sample to a database of Tox mean and non-2003-731472/69 **3** U e or cell, for ne expression and non-Tox

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Johnson

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Higgs

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Castle

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Claim 44; SEQ ID NO 3252; 874pp; English

comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyt toxicity modelling related gene sequence from the present invention. The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database rat hepatocyte state The

Sequence 1500 BP; 336 A; 408 C; 380 G; 376 T; 0 U; 0 Other;

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Query Match
Best Local Similarity
Matches 77; Conserv
Conservative
       18.1%;
98.7%;
0;
Score 76.4; D
Pred. No. 3.1e
0; Mismatches
        .1e-13;
                 멂
                 10;
Indels
                 Length
                 1500;
٥,
Gaps
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0

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RESULT 11
ABT41911
XX ABT41
XX ABT41
XX ABT41
XX ABT41
XX ABT41
XX Toxic
XX Toxic
XX Toxic
XX Toxic
XX Attl
AN Attl
XX Attl
AN Attl
XX Attl
AN Attl
An
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01-NOV-2001;
21-NOV-2001;
06-DEC-2001;
19-DEC-2001;
21-FEB-2002;
21-FEB-2002;
15-MAR-2002;
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10-JUL-2001;
28-AUG-2001;
27-SEP-2001;
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13-JUN-2001;
19-JUN-2001;
10-JUL-2001;
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08-APR-2002;
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2002US-0372794P.
2002US-0371679P.
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2002US-0357842P.
2002US-0357843P.
2002US-0357844P.
2002US-0364134P.
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2001US-0330867P.
2001US-0331805P.
2001US-0336144P.
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2001US-0303807P.
2001US-0303808P.
2001US-0303810P.
2001US-0315047P.
2001US-0324928P.
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2002US-0370206P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002WO-US016173
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                                                                                                                                                                                                                                                                                                                                                                                                                                        INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1613
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'n Porter M, Johnson ζ, Higge B, Castle Α Elashoff M;

WPI; 2003-148464/14.

Predicting at least one toxic effect of a compound, useful f modeling, comprises preparing a gene expression profile of a cell sample exposed to the compound, and comparing the gene profile to a database. for toxicity
a tissue or
e expression

Example 4; Page; 446pp; English.

The invention relates to a novel method of predicting at least one toxic effect of a compound. The method comprises a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising at least part of the data or information given in the specification. The methods are useful for predicting at least one toxic effect of a compound, predicting the progression of a toxic effect of a compound, predicting the renal toxicity of a compound, or identifying toxicity markers in tissues

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RESULT 12
ADP72689
ID 72689
ID 726-AU
XX ADP72
XX Renal
XX Adiffe
KW diffe
KW diffe
KW diffe
KW drug
KW focal
XX ACTU
PN WO200
XX Fattu
XX FOCAL
PN WO200
XX FATTU
PN WPI;
XX Menda
PI Elash
XX Menda
PI Elash
XX Menda
PI Elash
XX Pred:
PT monit
PT gene
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PT Compx
XX Pred:
PT Gene
CC toxic
CC toxic
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Best Local S
Matches 77
The invention relates to a method of predicting (the progression of) a toxic effect of a compound by preparing a gene expression profile of a kidney tissue or cell sample exposed to the compound and comparing the gene expression profile to a database, or detecting the level of gene(s) expression in a tissue or cell sample exposed to the compound, where differential gene expression compared to a control indicates a toxic effect (toxicity progression). The method is useful for predicting (the progression of) at least one toxic effect of a compound. The genes are useful as toxicity markers in drug screening and toxicity assays. The
                                                                                                                                                                                                             Claim 11;
                                                                                                                                                                                                                                                                  Predicting (the progression of) a toxic effect of a compound, for monitoring the progression of renal disease states, comprises preparing gene expression profile of a kidney tissue or cell sample exposed to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds; toxic effect; gene expression profile; kidney tissue; differential gene expression; toxicity progression; toxicity marker; drug screening; toxicity assay; kidney pathology; nephritis; kidney necrosis; glomerular injury; tubular injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cells exposed to known renal toxin. The genes are useful as toxicity markers in drug screening and toxicity assays, in monitoring disease or physiological states, or disease progression. This polynucleotide represents a rat DNA sequence relating to the toxic effect database described in the specification. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the World Intellectual Property
                                                                                                                                                                                                                                                                                                                                                                                                Elashoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-NOV-2002; 2002US-00301856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-NOV-2003; 2003WO-US037556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                        2004-460771/43.
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18-FEB-2000;
20-NOV-2000;
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                                                                                                                                                                                                                                                            Screening hepatotoxic expressing RISKMARKER with reference populat
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gould-Rothberg BE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CURA-) CURAGEN CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Dipippo VA,
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98.7%;
                                                                                                                                                                                                                                                      agent comprises contacting test cell population or INJURYMARKER with agent, comparing expression tion and identifying difference in expression
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1. No. 3.1e-13;
2. No. 3.1e-13;
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The present invention describes a method of screening a test agent for hepatotoxicity. The method comprises: (a) providing a test cell population comprising a cell capable of expressing one or more nucleic acid sequences selected from the group consisting of RISKWARKER 1-8 and the test cell population with a test

Disclosure;

Page

22-24;

76pp; English

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RESULT 14
ABN95896
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Best Local S
Matches 77
                     The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as
                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing and detecting the progression carcinoma or metastatic liver tumor in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease st disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agent; (c) measuring expression of one or more of the nucleic acid sequences in the test cell population; (d) comparing the expression of the nucleic acid sequence in the test cell population to the expression of the nucleic acid sequence in an reference cell population comprising at least one cell whose exposure status to a hepatotoxic agent in known; and (e) identifying a difference in expression levels of the RISKMARKER or INJURYMARKER sequences, if present, in the test cell population and reference cell population. The method is useful for identifying a hepatotoxic agent. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 2394; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-426119/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Horne D,
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                                                                                                                                                                                                                                                                                                                                                                                                                        Level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #2394 used to diagnose liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341 CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alvares C,
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98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                     of two or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peres-Da-Silva
   to monitor disease states,
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Pred. No. 4.8e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                               of liver cancer, hepatocellular patient, involves detecting the in a liver tissue sample.
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        WO200290580-A1
                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                                            Human IGFBP-1 gene sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         ABV75371
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                                                                                                                                                                                                                                                                                                                                          Insulin-like growth factor binding protein; IGFBP; cytostatic; liver;
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Search completed: September 1, Job time: 451.543 secs
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Best Local Similarity
Matches 141; Conserv
                                                                                                                                                                                                                                                                                                                                                                               The invention relates to detecting the presence or diagnosing the risk of a liver cancer in a patient. The method involves detecting in a biological sample obtained from the patient aberrant expression of a gene encoding an insulin-like growth factor binding protein (IGPBP). The method is useful for detecting the presence or diagnosing the risk of a liver cancer or for screening agents in a patient. The agent is useful for the manufacture of a medicament for treating and/or preventing liver cancer. The present sequence represents a human IGPBP-1 polypeptide encoding genomic DNA (GenBank Accession No. M74587)
                                                                                                                                                                                                                                                                                                                                                     Sequence 6128 BP; 1504 A; 1497 C; 1504 G; 1623 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting the presence or diagnosing the risk of a liver cancer in patient comprises detecting aberrant expression of a gene encoding insulin-like growth factor binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Page 104-108; 142pp; English.
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P-PSDB; ABB82757.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM nucleic - nucleic search, using sw model
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Homo	Sus	D76435 Homo sapien	BD000107 Different			CQ715195 Sequence	c	AC098668 Rattus no	Human	Papio	9 Homo	Homo		Hon		Par	AP000557 Homo sap	AP000556 Homo sapi	BX572096 Prochloro	AC143094 Macaca mu	AC143448 Macaca i	AC143451 Macaca	AC148209 Macropus	

RESULT 2 AR175909 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM	Db Qy	Query Match Best Local Matches 5	ORIGIN	FEATURES	COMMENT	TITLE JOURNAL	REFERENCE AUTHORS	ORGANISM	SOURCE	VERSION	ACCESSION	LOCUS	A57715
AR175909 194 bp DNA linear PAT 17-DEC-2001 Sequence 1 from patent US 6309878. AR175909 AR175909.1 GI:17917208 Unknown.	1 CATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 51	Query Match 100.0%; Score 51; DB 6; Length 194; Best Local Similarity 100.0%; Pred. No. 2.7e-06; Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps	/ organism="unidentified" /organism="unidentified" /mol_type="unassigned_DNA" /db_xref="taxon:32644"	Location/Qualifiers	INST NAT SANTE RECH MED (FR) Other publication AU 5652396 961030 Other mublication FD 2733978 961018	GLUCOSE-INDUCIBLE RECOMBINANT VIRAL VECTOR Patent: WO 9632489-A 1 17-OCT-1996;	1 Chen,R., Doiron,B. and Kahn,A.	unidentified unclassified.	unidentified	A57715.1 GI:3713539	١	A57715 194 bp DNA linear PAT 03-MAR-1998	
C-2001		0,										IR-1998	

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RESULT 3
E14395
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OS RATTUS NOTVEGICUS (rat)
PN JP 1997313059-A/14
PD 09-DEC-1997
PF 31-JAN-1997 JP 1997018966
PF 31-JAN-197 JP 1997018966
PF 
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Glucose-inducible recombinant viral vector
Patent: US 6309878-A 1 30-OCT-2001;
Location/Qualifiers
E14395.1 GI:5709078
JP 1997313059-A/14.
Rattus norvegicus (Norway rat)
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gDNA encoding pyruvate
E14395
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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/mol_type="unassigned DNA"
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Pred. No. 2.7e-06;
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; Murinae;
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                                                                                                     Boess, F., Suter-Dick, L. and Wolf, D. Methods for the toxicity prediction of a compound Patent: Ep 134484-A 36 17-SEP-2003, F. HOFFMANN-LA, ROCHE AG (CH)
                                                                                                                                                                                                     Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Sequence 36 from Patent EP1344834.
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7665. .7817,7911. .8077,
9298. .9479,10163. .11594)
                       /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product='Pyruvate
                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
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/number=7
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/number=5
6921. .7191
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7818. .791
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7302. .749
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Pred. No. 1.3e-06;
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intron 39495916	exon 3766. 3948	intron 32193765 /number=1	QLLSQYRPRAAVIAVTRSAQAARQVHLSRGVFPLLYREPPEAIWADDVDRRVQFGIES GKLRGFLRVGDLVIVVTGWRPGSGYTNIMRVLSVS"	IAREAEAAVYHRQLFEELRRAAPLSRDPTEVTAIGAVEASFKCCAAAIIVLTKTGRSA	IKIISKIENHEGVKKFDEILEVSDGIMVARGDLGIEIPAEKVFLAQKMMIGRCNLAGK PVVCATOMLESMTTKARDTRAETGNANAVLINGADCINLSGETAKGSFOVEAVMOHA	KGVNLPNTEVDLPGLSEQDLLDLRFGVQHNVDIIFASFVRKASDVLAVRDALGPEGQN	IREATESPATSPLSYRPVAIALDTKGPEIRTGVLQGGPESEVEIVKGSQVLVTVDPKF	LDIDSQPVAARSTSIIATIGPASRSVDRLKEMIKAGMNIARLNESHGSHEYHAESIAN	/db_xref="UniProt/Swiss-Prot: P12928" /translation="MEGGAGYIBDAGYANI TOGICTAN PEROCOOT BANKA TOTEL PUT OF	/db_xref="GOA:P12928"	/protein_id="CAA29169.1" /dh www.f="GT.297521"	/product="L-type pyruvate kinase"		CUS Join(32123218,37663948,59176008,61526283, 64186604,69217191,73027452,76657817,79118077,	n 3194. 3218		TATA_signal 31683173 precursor_RNA 319411594	1	ional	/note="direct repeat 2" repeat_region 14191434			/not	region	371		organism="Rattus norvegicus"		PUBMED	J. Mol. Biol. 196 (1), 11-25 (1987)	AUTHORS Cognet, M., Lone, Y.C., Vaulont, S., Kahn, A. and Marie, J. TITLE Structure of the rat L-type pyruvate kinase gene	REPERENCE 1 (bases 1 to 13011)	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	ש. כישהושלש. עסידיסקישלש.	pyruvate Rattus no	VERSION X05684.1 GI:56604	ACCESSION X05684	RNLPKG 13011 bp	RNLPKG		Db 3021 CATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 3071	1 CATAMAGA CACAMAGA TACAMAGA T	1 CAMACANANA CANANA CAN	No. 1.3e-06;	
ORIGIN	repeat_region	repeat_region	repeat_region	100000	polyA_site	repeac_region		repeat_region	repeat_region	excii		repeat_region	repeat_region	repeat_region		•	exon	intron	exon	intron		exon	intron	exon	11101011	101	exon	intron	exon		intron	exon	repeat_region	intron	exon	- 1	repeat region	repeat_region	repeat_region	1 () () () () () () () () () (7	repeat_region	repeat_region	repeat_region	
/note="direct repeat 8"		7	1261112654 /note="direct repeat 8"	/note="direct repeat 7"		/note="direct repeat 6"	/note="repetitive sequence 7"	7	1071210716	7.	/note="direct repeat 5"	crive seducine		95809588 /note="direct repeat 5"	er =	Ō	/number=9 92989479	80789297	79118077	78187910 /number=8	19	/number=7 76657817	7453 7664	73027452 /number=7	/number=6	6	/ Number = 5 69217191	6605 6920	64186604 /number=5	m	/number=4 62846417	/note="repetitive sequence 5" 61526283		60096151		IJ	/note="direct repeat 4" 54215500		/note="repetitive semience 1"	u	<pre>/note="direct repeat 3" 4536 4542</pre>	/noce="repectative sequence 2" 43884393		4066. 4071 4066. 4071 /note="direct repeat 3"	/number=2

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                        exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prim_transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                               intron
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M17088.1 GI:20
                                                                                                                                                                                                                             45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Original source text: Rat DNA (library of J.Bonner), clone lambda-LPK30, and reticulocyte, cDNA to mRNA, clones pRPK[1,3]. Draft entry and printed copy of sequence for [1] kindly provided by T.Noguchi, 09-SEP-1987.
  AC097039 231241 bp
Rattus norvegicus clone CH230-61E1,
                                                                                                                                                                                                                                                                                                                 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Noguchi,T., Yamada,K., Inoue,H., Matsuda,T. and Tanaka
The L- and R-type isosymes of rat pyruvate kinase are
a single gene by use of different promoters
J. Biol. Chem. 262 (29), 14366-14371 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pyruvate kinase.
1 of 4
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat pyruvate kinase
M17088 J03455
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                                                                                                                                                                                                                                                                                                             2191. .>2717
/note="PK intron B"
upstream of PstI site
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/mol type="genomic DNA"
/db xref="taxon:10116"
925. .>2717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="PK mRNA and introns (alt.)"
934. .>2717
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                                                                                                                                                                                                                                                                                                                                                                                 'number=2
                                                                                                                                                                                                                                                                                                                                                                                                                          note="PK intron A (alt.)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        number=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L-pyruvate kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="PK intron A"
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1080. .2007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene, exons 1 and
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Pred. No. 0.00059;
0; Mismatches 3
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Pred. No. 1.3e-06;
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    DNA linear HTG 10-MAY-2003
*** SEQUENCING IN PROGRESS ***
                                                                                                                                                                                                                                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 13011;
                                                                                                                                                                                                                                                                    Length 2717;
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                                                                                                                                                                                                                                                                                                                      MEZNY, J. Marlet, Metzker, M. Leer, Abramcon, S., Adams, C., Allen, C., Allen, H., Albbrocks, S., Amin, A., Angulanto, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barristead, M., Benahmed, F., Bladwin, D., Bandaranaike, D., Barber, M., Barristead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Brankenburg, K., Blyth, P., Brown, M., Brankenburg, K., Blyth, P., Brown, M., Buhay, C., Barch, P., Burrelli, K., Calderon, E., Chu, J., Charez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Charez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavazo, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Charez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chen, R., Chen, Y., Chen, Z., Chu, J., Chen, S., Dany, Carriol, A., Durbin, K., Duval, B., Baves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, M., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrier, M., Garza, M., Guerra, W., Ghuratthe, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Duval, B., Baves, K., Egan, A., Hernandez, J., Hernandez, R., Hines, S., Haddin, S.L., Hodgson, M., Hernandez, M., Hernandez, R., Hines, S., Haddin, S.L., Hodgson, M., Hernandez, M., Hernandez, R., Li, Z., Liu, J., Liu, Y., Loudon, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., Loudon, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., Loudon, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., Loudon, P., Longacre, S., Lopez, J., Liu, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, J., Liu, Y., London, P., London, P., Longacre, S., Lopez, J., Liu, J., Liu, J., Liu, Y., London, P., Martin, Z., Meenen, E., Lousey, M., Martin, R., Martin, R., Martin, R., Martin, R., Martin,
Submitted (10-MAY-2003) Human Genome Sequencing Center, Depay of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On May 10, 2003 this sequence version replaced gi:24819342.
                                                                                                                                      Submitted (06-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 231241)
                                                                                                                                                                                                                          Worley, K.C.
Direct Submission
                                                                                        Direct Submission
                                                                                                           Rat Genome Sequencing Consortium
                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED Rattus norvegicus (Norway rat)
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175858 GGCGCCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 175905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Totalia/Carlifers

* 1 231241: contig of 231241 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         table
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              shotgun sequence only contigs will be indicated in the feature
                                 GGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA
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Center project name: GHYF
Center clone name: CH230-61E1
Center Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 210827 bases at least Q40
Consensus quality: 214055 bases at least Q20
Consensus quality: 216056 bases at least Q20
Estimated insert size: 223098; sum-of-contigs estimation
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                                                                                                                     Conservative
                                                                                                                                                                                                                                                          /note="wgs_end_extension
clone_end:T7"
68569T.69982
/note="wgs_end_extension
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/clone="CH230-61E1"
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clone_end:T7
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|mol_type="genomic DNA"
                                                                                                                                              84.7%;
93.8%;
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                                                                                                                                              Score 43.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCTGGCATA 260
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 8409)

Lenzner,C., Nurnberg,P., Jacobasch,G. and Thiele,B.J.

Complete genomic sequence of the human PK-L/R-gene includes four intragenic polymorphisms defining different haplotype backgrounds of normal and mutent PK-genes

DNA Seq. 8 (1-2), 45-53 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           8409 bp DNA linear PRI 05-AUG-1999
Homo sapiens pyruvate kinase PK-R isoenzyme gene, partial cds; and
pyruvate kinase PK-L isoenzyme gene, complete cds.
U47654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39;
                                                                                         Submitted (30-JAN-1996) Peter Nuernberg, Institute for Medical Genetics, Charite Medical School of the Humboldt-University Be Schumannstr. 20/21, Berlin 10098, Germany
                                                                                                                                             2 (bases 1 to 8409)
Lenzner,C., Nuernberg,P., Jacobasch,G. and Thiele,H.-J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (03-DEC-1992) de Medicis
Biochimie, 12e avenue Nord, Fleurin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H.sapiens
Z18922
                                                                        Schumannstr. 20/21, Berlin 10098, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The promoter region Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                    9522120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    de Medicis, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter; pyruvate kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218922.1
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases-413-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Larochelle,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
db_xref="taxon:9606"
                   organism="Homo sapiens"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="liver pyruvate kinase promoter region"
/citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rref="genomic DNA"
xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.8%;
90.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and de Medicis,E.
region of human liver pyruvate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for liver pyruvate kinase promoter region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type="Leukocyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36.6; DB 9; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medicis E., Universite de Sherbrooke, Fleurimont, Quebec, Canada, J1H 5N4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 415;
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                                                                                                            Berlin,
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map="1q21"

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REFERENCE
AUTHORS
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VERSION
                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
AY316591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                       FOCUS
                                                                                                                                                                                                                        ŒYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                     ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39;
Rieder, M.J., Livingston, R.J., Daniels, M.R., Montoya, M.A., Chung, M.-W., Miyamoto, K.E., Nguyen, C.P., Nguyen, D.A., Poel, C.L., Robertson, P.D., Schackwitz, W.S., Sherwood, J.K., Witrak, L.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 13322)
                                                                                                                                                                                                                                                AY316591.1
                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                           AY316591
                                                                                                                                                                                                                                                                                                                                                     AY316591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCTGGCATA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MPLTTQQCGADPQRGRPREVCSGMEGPAGYLRASVAQLTQELG
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GGPESEVELVKGSQVLVTVDPAFRTRGWANTVWVDYPMIVAVVPVGGRIYIDDGLISL
VQKIGPEGLVTQVENGGVLGSRKGVNLPGAQVDLPGLSEQDVRDLRFGVEHGVDIVF
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EIPAEKVFLAQKOMMIGRUNLAGKPVVATYGNLESMITKPFTRAETSDVANAVLDGAG
CIMLSGETAKGNPPVEAVKMQHAIAREABAAVHRQLFEELRRAAPLSRDPTEVTAIG
AVEAAEKCCAAAIIVLTTTGRSAQLLSRYRPBAAVLAVTRSAQAARQVHLCRGVFPLL
READAFKCCAAAIIVLTTTGRSAQLLSRYRPBAAVLAVTRSAQAARQVHLCRGVFPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="hsmvpqpqahtesmsiqenissiqlrsmvsksqrdlaksiliga
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Ilatigpasseverlkemikagmniarlnfsshsyleyhagatts
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NIVRVPVGGRIYIDDGLISLVVQKIGPEGLVTQVENGGVLGSRKGVNLPGAQVDLPG
NISQDVRDLRFGVEHGVDIVFASFVRKASDVAAVRAALGPEGHSKIISKIENHEGVK
RFDEILEVSDGIMVARGDLGIEIPAEKVFLAQKMIGRCHLAGKFVVCATQMLESMIT
KPRFTEAETSDVANAVLDGADCIMLSGSTAKGNFPUEAVKMOHAIAREAEAAYYHRQL
FEELRRAAPLSRDPTEVTAIGAVEAAFKCCAAAIIVLTTTGRSAQLLSRYRPRAAVIA
VTRSAQAARQVHLCRGVFPLLXREPPEAIWADDVDRRVQFGIESGKLRGFLRVGDLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YREPPEAIWADDVDRRVQFGIESGKLRGFLRVGDLVIVVTGWRPGSGYTNIMRVLSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="pyruvate kinase PK-L isoenzyme"
join(478. .553,1145. .1327,2508. .2599,2696. .2827,2961. .31
3510. .3780,3877. .4027,4672. .4824,4919. .5085,6325. .6506,
7572. .7678)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(<478. .553,1145. .1327,2508. .2599,2696. .2827,
2961. .3147,3510. .3780,3877. .4027,4672. .4824,4919.
6325. .6506,7572. .7678)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="pyruvate kinase PK-R isoenzyme"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="pyruvate kinase PK-L isoenzyme"
/protein_id="AAA92536.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVTGWRPGSGYTNIMRVLSIS"
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3510. .3780,3877. .4027,4672. .4824,4919. .5085,6325. .6506,
7572. .>7678)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                              GI:32140478
                                                                                                                                                                                                                                                                                                                       pyruvate kinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36.6; DB Pred. No. 0.068; O; Mismatches
                                                                                                                                                                                                                                                                                                                       13322 bp DNA linear inase, liver and RBC (PKLR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.
                                                                                                                 Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 8409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                    gene, complete
                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                  PRI 21-JUN-2003
                                                                                                                 Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .3147,
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
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        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
                                                                                                              variation
                                                                                                                                                                                                                   variation
                                                                                                                                                                                                                                                                                      repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (06-JUN-2003) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA
To cite this work please use: NIEHS-SNPs, Environmental Genome Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="pyruvate kinase, liver and RBC"
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RIKKEMIKAGMNIARLMFSHGSHEYHAESIANVERAVESFAGSPLSYRPVALALDTKGP
ERFGILQGGPESEVELVKGSQVLJTYDDAFRTRGNANTTWWDYKUIVRVPVGGRIY
IDDGLISLVVQKIGPEGLVTQVENGGVLGSRKGVNLPGAQVDLPGLSEQDVRDLRFGV
EHGYDIVFASFVRKASDVAAVVAALGPEGHGIKIISKIEMHEGVURFDEILEVSDGIM
VARGDLGIEIPAEKVFLAQKOMNIGRCNLAGKPVVCATQMLESMITKERFTRAETSDVA
NAVLDGADCIMLSGETAKGNFFVEAVKMQHAIAREAEAAVYHRQLFEELLRRAAPLSRD
PTEVTAIGAVEAAFKCCAAAIIVLTTTGGRSAQLLSRYRRAAVIAVTRAGARGVHL
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2081. .4840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1346. .156/
/rpt_family="MIR"
                                                                                                                                                                                                                                                                                              1951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRGVFPLLYREPPEAIWADDVDRRVQFGIESGKLRGFLRVGDLVIVVTGWRPGSGYTN
                                                                                                                                                                                                                                                                                                                 frequency="0.02"
replace="a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(<525. .649,1665. .1847,6189. .6280,6377. .6508,
5643. .6829,7193. .7463,7560. .7710,8355. .8507,8602. .8768,
,0008. .10189,11267. .11691)
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                                                                                                                                                                                          gene="PKLR"
                                                                                                                                                                                                                                                                                                                                                                          'gene="PKLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MRVLSIS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="PKLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              frequency="0.01"
replace="t"
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/db_xref="taxon:9606"
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                                                        frequency="0.42"
                                                                                      gene="PKLR"
                                                                                                                                    replace="t"
                                                                                                                                                            frequency="0.03"
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/rpt_family="Alu"
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7113
 /gene="PKLR"
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                                                                                                          REFERENCE
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AL713999/c
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                                                     Submitted (13-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On May 14, 2003 this sequence version replaced gi:30523877.
                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 133525)
                                                                                                                                                                                                                                                    sequence.
AL713999
                          Center: Wellcome Trust Sanger Institute Center code: SC
                                                                                                                                                                                                                                                                            AL713999 133525 bp DNA linear PRI Human DNA sequence from clone RP11-263K19 on chromosome
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                          Direct Submission
                                                                                                                                                                                                           Homo sapiens (human)
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nilarity 90.7%;
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Pred. No. 0.063;
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JOURNAL
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                                              Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W.,
Bouffard, G.G., Brinkley, C., Brooke, S., Chu, G., Coleman, B.,
Coleman, H., Daki, N., Engle, J., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B.,
Idol, J.R., Jones, C., Karlins, E., Kim, H., Kwong, P., Laric, P.,
Larson, S., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B.,
Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J.,
Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J.,
Margulies, B., M., Schandler, K., Schueler, M.G., Shah, K., Sison, C.,
Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C.,
Scantripop, S., Thomas, J. W., Thomas, J. J., Tsipouri, V., Vogt, J.L.,
Wetherby, K.D., Young, A. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1

RP11-263X19 is from the library RPCI-11.1 constructed by the group of pierer de Jong For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC148047
AC148047.2 GI:45544599
HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
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                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur 1 (bases 1 to 192549)
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Otolemur garnettii clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Otolemur garnettii (small-eared galago)
                          Comparative Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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/clone_lib="RPCI-11.1"
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/chromosome="1"
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Pred. No. 0.041;
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                                                                                      Vogt, J.L.,
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db_xref="taxon:30611" mol_type="genomic DNA"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (18-MAR-2004) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Mar 18, 2004 this sequence version replaced gi:41386816.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Green, E.D.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with a Phrap-derived quality score.
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                                                                                                                                                                                                                                                                                                                                          This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 38219: contig of 38219 bp in length 38220 38319: gap of unknown length 198219: contig of 38900 bp in length 198219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                             114116
114216
126275
126375
152698
152798
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                                                                                167007
                                                                                                                                                                                                                                                                                              38220
38320
77220
77320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 190022 bases at least Q40
Consensus quality: 191157 bases at least Q30
Consensus quality: 191179 bases at least Q20
Insert size: 149000; agarose-fp
Insert size: 191949; sum-of-contigs
Quality coverage: 11.55x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: nisc_zoo@nhgri.nih.go
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.nisc.nih.gov
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                                                       Location/Qualifiers
organism="Otolemur garnettii"
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192549:
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                                                                                                                               gap of unknown length contig of 26323 bp in gap of unknown length contig of 14109 bp in
                                                                                                                                                                                                                                      gap of unknown length contig of 36796 bp in gap of unknown length contig of 12059 bp in
                                                                             gap of unknown contig of 25543
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AC147942/c
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                                                                                                                                                                                                                                                                                      Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B., Coleman, H., Daki, N., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B., Idol, J.R., Jones, C., Karlins, E., Kim, H., Kwong, P., Laric, P., Larson, S., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Mullikin, J.C., Paguirigan, C., Portnoy, M.E., Prasad, A., Puri, O., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Matherby, K.D., Young, A. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                   Submitted (18-MAR-2004) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Mar 18, 2004 this sequence version replaced gi:41058168.
                                                                                                                                            Submitted (22-JAN-2004) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA (bases 1 to 95718)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC147942.2 GI:45544627
HTG; HTGS_PHASE2; HTGS_DRAFT.
Carollia perspicillata (Seba's short-tailed bat)
Carollia perspicillata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carollia perspicillata clone
                                                                                                                            Green, E.D.
                                                                                                                                                                                                                                   Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
Carollinae; Carollia
1 (bases 1 to 95718)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ordered pieces.
                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                       unpublished
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                                                                                                                                                                                                                                                   (bases 1 to 95718)
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Center: NIH Intramural Sequencing Center
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126375. .152697
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81.2%;
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≥ 47203,
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WORKING DRAFT SEQUENCE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 18809 18908: contig of 18808 bp in length

* 18909 22119: contig of 3211 bp in length

* 22120 2219: gap of unknown length

* 22220 31750: contig of 9531 bp in length

* 31751 31850: gap of unknown length

* 31851 53063: contig of 9531 bp in length

* 53164 95718: contig of 21213 bp in length

* 53164 95718: contig of 42555 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 94695 bases at least Q40 consensus quality: 95070 bases at least Q30 Consensus quality: 95243 bases at least Q20 Insert size: 95100; agarose-fp Insert size: 95108; sum-of-contigs Quality coverage: 11.88x in Q20 bases; sum-of-contigs Quality coverage: 11.15x in Q20 bases; sum-of-contigs
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Center clone name: 472003
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                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment
clone_end:SP6
vector_side:left"
                                                                 53164. .95718
                                                                                                                                  31851.
/note="assembly_fragment
clone_end:T7
                                                                                                                                                                                         /note="assembly_fragment"
22220. .31750
                                                                                    /note="assembly_fragment"
                                                                                                                                                                                                                                                       18909.
                                                                                                                                                                                                                                                                             /note="clone overlaps with GenBank Accession Number AC148052 clone 593F8 (center project name gda)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="The Green Lab"
/note="egreen@nhgri.nih.gov"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA
/db_xref="taxon:40233"
/clone="47203"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Carollia perspicillata"
/mol_type="genomic DNA"
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AC147944/c
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                                                                                                                                   The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8x average.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B., Coleman, B., Daki, N., Bigle, J., Granite, S., Guan, X., Gupta, J., Coleman, P., Daki, N., Hansen, N., Ho, S.-L., Hu, P., Hurle, B., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B., Idol, J.R., Jones, C., Karlins, E., Kim, H., Kwong, P., Laric, P., Larson, S., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Maslello, C., Maskeri, B., McDowell, J., Margulies, E.H., Maslello, C., Maskeri, B., McDowell, J., Margulies, P., Schandler, K., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Nick, Company, A. and Green, E.D.
                                           coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (18-MAR-2004) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Mar 18, 2004 this sequence version replaced gi:41058180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (22-JAN-2004) NIH Intramural Sequencing Center,
Grovemont Circle, Gaithersburg, MD 20877, USA
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HTG; HTGS PHASE2; HTGS DRAFT.
Atelerix albiventris (middle-African hedgehog)
Atelerix albiventris
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Atelerix albiventris clone LB4-218C14, WORKING DRAFT SEQUENCE, 9
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                                                                                                                                                                                                                                                                                                                                                                        Center project Information Center project name: dut Center clone name: 218C14
                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
Sequencing vector: plasmid; n/a; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: NIH Intramural Sequencing Center code: NISC
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    Summary Statistics

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Pred. No. 1
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ORIGIN
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106462
125086
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86150
96129
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* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1743 contig of 7473 bp in length

* 7574 17573: gap of unknown length

* 12023 12122: gap of unknown length

* 12023 12122: gap of unknown length

* 12123 37423: contig of 25301 bp in length

* 37524 54271: contig of 16748 bp in length

* 37524 54271: gap of unknown length

* 37524 54271: gap of unknown length

* 54372 86049: contig of 31678 bp in length

* 54370 86149: contig of 31678 bp in length
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This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 135309 bases at least Q40
Consensus quality: 135732 bases at least Q30
Consensus quality: 135745 bases at least Q20
Insert size: 144000; agarose-fp
Insert size: 136083; sum-of-contigs
Quality coverage: 12.45x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                               61666. .136883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone_end:SP6
clone_end:T7
                                                                      106462. .125085 /note="assembly_fragment"
                                                                                                                                                                       96229. .106361
                                                                                                                                                                                                                               86150. .96128
                                                                                                                                                                                                                                                    /note="clone overlaps with GenBank Accession Number
AC148054 clone LB4-124B14 (center project name dus)
                                                                                                                                                                                                                                                                                                                                                                            54372. .86049
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/mol_type="genomic DNA"
/db_xref="taxon:9368"
                                                          125186. .136883
                                                                                                                                                                                      /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                           note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment"
12123. .37423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment
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AC148055 clone LB4-416H21 (center project name duv)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="LB4-218C14"
/clone_lib="LB4"
/note="BAC resource: http://bacpac.chori.org/"
                    note="assembly_fragment
                                                                                                                              note="assembly_fragment"
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s: contig of 9979 bp in length
gap of unknown length
contig of 10133 bp in length
contig of 10133 bp in length
contig of 16264 bp in length
contig of 18674 bp in length
gap of unknown length
gap of unknown length
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                                                                                                                       The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in O20 bases and has been reviewed to rule out gross misssemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated
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Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B.,
Coleman, H., Daki, N., Engle, J., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B.,
Idol, J.R., Jones, C., Karlins, E., Kim, H., Kwong, P., Laric, P.,
Larson, S., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B.,
Margulles, E.H., Masiello, C., Maskeri, B., McDowell, J.,
Margulles, E.H., Masiello, C., Maskeri, B., McDowell, J.,
Mullikin, J.C., Paguirigan, C., Portnoy, M.E., Prasad, A., Puri, O.,
Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C.,
Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L.,
Wetherby, K.D., Young, A. and Green, E.D.
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AC148054.<sup>2</sup>
GI:46250790
HTG; HTGS PHASE2; HTGS DRAFT.
Atelerix albiventris (middle-African hedgehog)
Atelerix albiventris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (07-APR-2004) NIH Intramural Sequencing Center, Grovemont Circle, Gaithersburg, MD 20877, USA On Apr 7, 2004 this sequence version replaced gi:41386823
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Atelerix albiventris clone LB4-124B14, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (29-JAN-2004) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
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Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ordered pieces.
                                                                                                         with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Green, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 153222)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 153222)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 153222)
                        Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: nisc zoo@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: dus
Center clone name: 124B14
Assembly program: Phrap; version 0.990319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: NIH Intramural Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submission
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Pred. No. 5;
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139917
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* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* the accession number will be preserved.

* 889 contig of 888 bp in length

* 989 gap of unknown length

* 2430 24329: contig of 23341 bp in length

* 2433 33974: contig of 9545 bp in length

* 33975 34074: gap of unknown length

* 34075 48829: contig of 10755 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  consists of 12 contigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         are represented as runs of N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 150788 bases at least Q40 consensus quality: 151405 bases at least Q30 consensus quality: 151850 bases at least Q20 Insert size: 126000; agarose-fp Insert size: 152122; sum-of-contigs Quality coverage: 12.62x in Q20 bases; sum-of-cont Quality coverage: 10.45x in Q20 bases; sum-of-cont
                                                                                                                                                                                                                                                                                                                                                                                                                                  vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_end:T7
                                                                                                                                                                                                                                                                                                                      34075. .44829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC147944 clone LB4-218C14 (center project name dut)"
                           /note="assembly_fragment"
106506. .139816
                                                                                                                                                                                                                                                                      44930.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="LB4-124B14"
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|note==BAC resource: http://bacpac.chori.org/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Atelerix albiventris"
| mol_type="genomic DNA"
note="assembly_fragment"
                                                                                                                                                                                                                                note="assembly_fragment"
                                                                                                                                                                                                                                                                                        note="assembly_fragment"
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                                                                                          note="assembly_fragment
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db_xref="taxon:9368"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type="genomic
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9: contig of 17267 bp in length
9: gap of unknown length
1: contig of 12762 bp in length
1: gap of unknown length
5: contig of 2434 bp in length
5: gap of unknown length
5: gap of unknown length
6: contig of 33311 bp in length
6: contig of 33311 bp in length
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---ntig of 4671)
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of 8535
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Search completed: September 1, 2005, 03:26:37 Job time: 327.549 secs
                                                                                                                                                                                                     ORIGIN
                                                                                                                                 Query Match 59.2%; Score 30.2; DB 2; Length 153222; Best Local Similarity 81.4%; Pred. No. 4.9; Matches 35; Conservative 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                 misc_feature
                                                                139917. .148451
/notee=massembly_fragment=
148552. .153222
/notee=massembly_fragment
clone_end:SP6
vector_side:right=
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Result
No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM nucleic - nucleic search, using sw model
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    2222111111111
43210987654
                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                              Score
   987654321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    August 31, 2005, 20:18:35 ; Search time 387.736 Seconds (without alignments) 5006.706 Million cell updates/sec
                                                                                                                                                                                                                Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                            34239544 seqs, 19032134700 residues
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Gapop 10.0 , Gapext 1.0
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51
   EST:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                       9b est1:
9b est2:
9b est3:
9b est3:
9b est4:
9b est6:
9b est6:
9b est6:
9b est8:
9b est8:
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   DB
         AZB40793
BMZ86930
BP1J0536
BEB67300
BP1J05350
CES128750
CES13055
CCE450351
CCH450351
CDB30056
CDB30056
CDB30056
CDB30056
CDB30056
CDB30057
CCH4503282
BM056161
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BM106634
BG106634
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BG404685
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AZ840793 ZM0138D02
BM286900 527229 MA
BF105536 601822455
BE867308 601442381
AL528750
CE316355 tigr-988-
CE450351 tigr-988-
CE450351 tigr-988-
CE0530055 560279324
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AW925227 DG1_17
B0056161 AGENCOURT
AW925227 DG1_17
B0056161 RC5-RT005
CE745382 ZMMBE034
B1006710 RC5-RT005
CE744237 tigr-988-
AW577607 PM2-BT055
BU186634 AGENCOURT
BG48205 GGAAW77TC
BG438699 AGENCOURT
CE608928 tigr-988-
CE555764 tigr-988-
CE555764 tigr-988-
BF189053 234314 MA
AU079412 AU079412
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610	595	594	572	569	552	541	539	528	523	521	518	469	442	413	377	267	265	913	899	884
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CE256374	CE123626	CK619547	CE075799	BM944273	CE668350	CK627560	BM943713	CN670899	CE338459	BM944811	CN669363	CE699841	CE200317	CO739485	CB177707	CG481325	CE418242	BQ940337	CC972844	PETOTORI
CE256374	CE123626	CK619547	CE075799	BM944273	CE668350	CK627560	BM943713	CN670899	CE338459	BM944811	CN669363	CE699841	CE200317	CO739485	CB177707	CG481325	CE418242	BQ940337	CC972844	TRCTOTAR
tigr-gas	tigr-ges-	mk25e02.y	tigr-gas-	UI-M-EHOP	tigr-gas-	io05f01.y	UI-M-EHOP	A0898H12-	tigr-gas-	UI-M-EHOP	A0878H10-	tigr-ges-	tigr-gee-	S1LB06a23	in94f04.x	OST13706	tigr-gss-	AGENCOURT	ZUACY29TH	96 F C C / TO9

ALIGNMENTS

												_																
	source	FEATURES									COMMENT	JOURNAL	1	TITLE			AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	MOTSSSCOM	DEFINITION	Locus	RESULT 1	
/organism="Mus musculus" /mol_type="genomic DNA" /strain="C578L/6J" /db_xref="taxon:10090" /db_xref="taxon:10090" /clone="UUGC2M0138D02" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /lab_host="Mouse 10kb plasmid UUGC1M library" /clone_lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: PW042nv; Purified genomic DNA from M. musculus C578L/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA	1 659	night quairly sequence scop: 639.	Seg primer: (ACACAGGAAAACAGCTATGACC Class: plasmid ends	Plate: 0138 row: D column: 02	Insert Length: 10000 Std Error: 0.00	Fax: 801 585 7177	Tel: 801 585 5606	RMI. 308, BIOMEDICAL FOLYMERS RESEARCH BIOG., 20 S. 2030 B., SEC, OF 84112, USA	מינים מינים לינים	University of Utah Genome Center	Contact: Robert B. Weiss	Unpublished (2000)	plasmid inserts	Mouse whole genome scaffolding with paired end reads from 10kb	Niederhausern A and Wright D Weine R	Islam, H., Longacre, S., Manmoud, M., Meenen, E., Pedersen, T.,	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,	1 to 659)	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Mus musculus	Mus musculus (house mouse)		AZ840793.1 GI:13010701	Cione Dugczmuisbuuz k, genomic survey sequence.	8 mus	AZ840793 659 bp DNA linear GSS 20-FRB-2001		

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PUBMED COMMENT
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BM286990
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ACCESSION
                                                                                                                                                                                                                                          FEATURES
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
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527229 MARC 3BOV Bos tau:
BM286990
BM286990.1 GI:17996016
EST.
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Chackenbush, J. and Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 51
                                                                                                                                                                                                                                     Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                         FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                  Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with
v0.989904.e. Vector identified by cross_match with the -mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                       Plate: 135 row: G column:
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                                                                                                                                                                                                                                                                                                                                                                  PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                            -minmatch 12 options.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MARC 3BOV Bos taurus cDNA 5',
                                                                                /mol type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone lib="MARC 3BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from marrow, alveolar
                                                                                                                                                                                    organism="Bos taurus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLCM871 row: m column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Ir
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 827)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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                                                                                                                             Conservative
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longissimus
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78.6%;
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75.0%;
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Pred. No. 29
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On reward. Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer: Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL528750 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo CDNA Clone CSODD001YN07 3-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                          Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 765)
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Plate: LLM9559 row: a column: 22
High quality sequence stop: 563.
Location/Qualifiers
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BE867308.1 GI:10316084
                                                                                                                                                                                                                       On Feb 13, 2001 this sequence version replaced gi:31066600
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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AL528750.3 GI:45703809
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Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
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National Institutes of Health, Mammalian Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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/lab host="DH10B (phage-resistant)"
/clome_lib="NIH_MCC_65"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo d'Average insert size 1.8 kb. Library constructed by Li Technologies. "
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/mol_type="mRNA"
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75.0%;
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Best Local Similarity
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                    μ
                                                        l Similarity
30; Conser
                                                                                                                                                                                                                                                                                                                                                                                 The Institute for Genomic Research Department of Eukaryotic Genomics, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomic survey sequence CE316355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CATGGGCGCACGGGCACTCCCGTGGTTCCTGGACTCTGGCC 42
                                                                                                                                                                                                                                                                                                                                               Tel: 301-838-0200
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canis familiaris (dog)
Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tigr-gss-dog-17000361087224
                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Kirkness EF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             14512627
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Location/Qualifiers
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CATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTC
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                                                                                                                                                                                                                                                                                                               shotgun.
                                                                                                                                                                                                                                                                                                                                ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED" /clone_lib="HOMO sapiens NEUROBLASTOMA COT 50-NORMALIZED" /note="Tast strand cDNA was primer with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                            /clone lib="Dog Library"
/note="Site_1: BstXI; Libraries were prepared from
peripheral blood"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODD001YN07"
                                                                                                                                                                                                                    organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                     db_xref="taxon:9615"
                                                                       50.6%;
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Pred. No. 2.7e-
0; Mismatches
                                                      Score 25.8; DB 9;
Pred. No. 3e+02;
D; Mismatches 7;
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CATGGGCACAGTGGGCACTCCCGGCCGTCCCTGGCCTC

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JOURNAL COMMENT
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AUTHORS
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VERSION
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CN360924/c
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JOURNAL
MEDLINE
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                                                                                         HITLE
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                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 739)

Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.

Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
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 Geron Corporation 230 Constitution 1
                            Contact: Brandenberger R
Regenerative Medicine
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CN360924.1
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17000470668057 GRN_EB Homo sapiens
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Fax: 301-838-0208
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The Institute for Genomic
Department of Eukaryotic G
Rockville, MD 20850, USA
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Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
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CE450351
CE450351.1 GI:36740297
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                                                                                                                                                                                             Homo sapiens (human)
Homo sapiens
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
1. (bases 1 to 672)
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Constitution Drive,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Dog_Library"
/note="Site_1: BstXI; Libraries were prepared
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="Standard Poodle"
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mol type="genomic DNA"
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Pred. No. 3.1e-
0; Mismatches
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Park,
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CDNA 5', mRNA sequence.
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CA 94025,
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Canis.
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CD630056
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LOCUS
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CD630055/c
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56027932H1 I
CD630055
CD630055.1
EST.
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1 (Dases 1 to 225)

Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.

Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

extension cloning of partial genes

Genomics 84 (1), 205-210 (2004)
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Contact: Fu GK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD630056.1 GI:40278322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3160 Porter Dr., Palo Alto, CA 94304, Tel: 6508454102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Fax: 650 473 7760
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: gfu@incyte.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Incyte Genomics, Inc.
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Insert Length: 739 Std Error: 0.00
                                                                                                                                                                GCACGTGGACCACCCGGGGAGCCTGGACTCTGGCATCCAG 124
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                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol type="mRNA,"
/db_xref="taxon:9606"
/clome 11b="FLP"
/note="Vector: pDrive Cloning Vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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FLP Homo sapiens cDNA,
                    GI:40278321
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cDNA,
                                                    mRNA sequence
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REFERENCE
AUTHORS
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BQ056161/c
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5', mRNA Bequence.
BQ056161
BQ056161 GI:19815501
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1021)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. a Circular rapid amplification of cDNA ends extension cloning of partial genes Genomics 84 (1), 205-210 (2004)

Contact: Fu GK
                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 229)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                   Plate: LLCM2052 row: h column: 18
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                                                                                                                                                                                                                                                                                                                      nttp://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL
                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAG 47
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                                                                                                                                                                                                                                                                               quality sequence
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/tissue_type="lymphoma, cell line"
/lab host="DH10B (phage resistant)"
/clone_lib="NIH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
                                                                                                                                                                clone="IMAGE:5808449"
                                                                                                                                                                                      db xref="taxon:9606"
                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                             ity sequence stop: 669
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="FL|
/note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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77.5%;
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ls for high-throughput
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VERSION
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CC453282/c
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Best Local Similarity
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                                                                                                                                            459 GTGCACACGGGGCACTCGAGCAGCTCGTGAACGCTGGTCGCCGGTG
ZMMBBC0344B20r :
genomic survey :
CC453282
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DG1_17_E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 472)
                                                     CC453282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sorghum bicolor (sorghum)
Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: JEN REV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C.,
                                                                                                                                                                GGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTG 49
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                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                             /clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/notes"Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site 1: XhOI; Site 2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II
Clones to be sequenced were prepared by mass excision."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          'mol_type="mRNA"
'db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Sorghum bicolor"
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                                                                                                                                                                                                            Score 25.2; DE Pred. No. 4.8e+ 0; Mismatches
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(DG1) Sorghum bicolor cDNA,
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                                    clone ZMMBBc0344B20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34;
                                                                                                                                                                                             1 (bases 1 to 334)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       w
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI006710 334 bp mRNA linear RC5-RT0053-110101-011-H09 RT0053 Homo sapiens cDNA,
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Rese
Rua Prof. Antonio Prudente 109,
                                         Contact: Simpson A.J.G. Laboratory of Cancer Ge
                                                                                10737800
                                                                                                                       Proc. Natl.
                                                                                                                                     sequence tags
                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                               Simpson, A.J.
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Class: BAC ends
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Fax: 732 445 5735
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                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Bharti, A.K.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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1 (bases 1 to 259)
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Location/Qualifiers
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CE744237/c
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VERSION
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Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canis familiaris (dog)
Canis familiaris
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tigr-qss-dog-17000369534847 I
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-RT0053-
110101-011-H09&t3=2001-01-11&t4=1)
Seq.primer: puc 18 forward
Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                             Contact: Kirkness EF
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                           The dog genome: survey sequencing and comparative analysis considered 301 (5641), 1898-1903 (2003)
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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Location/Qualifiers
                                                                                                                                                                                                                               Fax: 301-838-0208
                                                                                                                                                                                                                                                     Tel: 301-838-0200
                                                                                                                                                                                                                                                                    Department of Eukaryotic Rockville, MD 20850, USA
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                                                                                                                                                                                      shotgun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: kidney_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini_library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
peripheral
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               'clone_lib="Dog Library"
'note="Site_1: BstXI; Libraries were prepared from
                                                                                                                                                              ocation/Qualifiers
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Query Match

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1: geneseqn1980s:*
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Listing first 45 summaries
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Compugen Ltd.
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is derived by analysis of the total score distribution.

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52.9 51.0 48.2 48.2 47.8 47.8	100.0 94.1 94.1 58.8 52.9	100.0	% Query Match
27 26 55001 55001 3138 3138 3138	13011 48 51 30 27	51 194 270 321 372 423 13011 13011	% Query Match Length
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ADE83566 ADE83614 ADG88848 ADH74825 AAA62683 ABN95218 ADN04235	ADP72914 ABX15379 ABX15380 ADE83565 ADE83567	ABX15371 AAT43002 ABX15373 ABX15374 ABX15375 ABX15376 ABX15376 ABX15376 ABX15376	SUMMARIES
രജ	Adp72914 Renal toox Abx15379 Rat liver Abx15380 Rat liver Ade83565 ChREBP pu Ade83567 L-pyruvat	Abx15371 Rat gluco Abx13002 Rat type Abx15373 Rat insul Abx15375 Rat insul Abx15375 Rat insul Abx15376 Rat insul Abx15376 Rat insul Abx16331 CDNA enco Abt42448 Toxicity	Description

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AAK77581	AAS35064	AAS30237	AAS28996	ADF70603	AAH78712	AAI99548	ABT17029	ABZ42551	AAS98070	AAV38513	AAK77579	ACC84331	AAI68793	ADO29943	ABZ42892	ABV73365	AAS98133	AAK77580	ACH79332	ACH93032	AAT43003	ADQ22099	ADR25048	ADQ17359
Aak77581 Human imm	Aas35064 DNA #14	Aas30237 DNA encod	Aas28996 Genomic	Adf70603 Orphai	Aah78712 Human EX3	Aai99548 Human exp	Abt17029 Human MP2	Abz42551 Human G p	Aas98070 Human DNA	Aav38513 Human 7-t	Aak77579 Human imm	Acc84331 Human hpl	Aai68793 Human M	Ado29943 Human GPC	Abz42892 Human GPC	Abv73365 Human TGR	Aas98133 Human DNA	Aak77580 Human imm	Ach79332 Human gen	Ach93032 Human gen	Aat43003 Rat type	Adq22099 Human sof	Adr25048 Breast ca	Adq17359 Human sof

ALIGNMENTS

ABX15371;

ABX15371 standard; DNA;

51 BP

RESULT 1
ABX15371
IID ABX11
XX ABX11
XX ABX1
AC ABX1
XX TO ABX1
XX Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatcoyte; hepatcoma; cellular protein degradation; antidiabetic; intracellular hormone receptor; insulin regulator construct; anabolic. 08-AUG-2002 Rattus norvegicus. Rat glucose response element (GIRE) DNA. 10-OCT-2001; 2001US-00972916 US2002107198-A1. 17-APR-2003 (first entry)

11-OCT-2000; 2000US-0239113P

(THUL/) THULE P M.

WPI; 2002-674190/72.

New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insuliver cells. ingulin 'n

Claim 7; Page 13; 37pp; English.

The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like gr growth

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ARESULT 2
AAT43002
ID AAT4
XX AAT4
XX AAT4
XX AGLA
AC AAT4
XX Gluc
XW Gluc
XW Hype
KW SS.
XX Ratt
XX EFT Prom
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                                                                                      Recombinant defective virus contg. heterologous gene under control of glucose inducible promoter - and infected mammalian cells, esp. for g
                                                                                                                                                                                          WPI; 1996-477139/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor binding protein-1 (IGFBP-1) basal promoter. The construct
                                                                                                                                                                                                                                                ₽,
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                                                                   of.
                                                                                                                                                                                                                                                                                                          INST NAT SANTE & RECH MEDICALE
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                                                                                                                                                                                                                                             Doiron B,
                                                                diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                          95FR-00004558
                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-FR000560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diabetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= L4_element
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                                                                                                                                                                                                                                                    Kahn
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"able to in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pyruvate kinase type L; L-PK;
s; gene therapy; viral vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВÞ
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interact with
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Claim 4;

Page 21; 41pp; French

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (GISE) of an insulin-like growtl factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glucose response element; GRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A new defective recombinant virus contains at least one heterologous gunder control of an expression signal inducible by glucose or its analogues. Preferably, the expression signal is derived from the 183 k region located 5' of the type L pyruvate kinase (L-PK) gene, especiall having the present sequence. Expression of the recombinant virus can k controlled by glucose levels, but insulin production can be stopped immediately by administering glucagon. This avoids the risk of hypoglycaemia caused by excessive insulin production. Mammalian cells infected by the virus can be implanted into liver, spleen, pancreas or intestine, to provide insulin secretion at predetermined sites. The virus full is provided insulin secretion at predetermined sites. The virus can be implanted into liver, spleen, pancreas or intestine, to provide insulin secretion at predetermined sites. The virus can be stopped to the virus can be implanted into liver, spleen, pancreas or intestine, to provide insulin secretion at predetermined sites. The virus can be stopped to the virus can be implanted into liver.
                                                                                                        The invention relates to
                                                                                                                                             Claim 9; Page 13-14; 37pp; English.
                                                                                                                                                                                                         New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insu
                                                                                                                                                                                                                                                                       WPI; 2002-674190/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 194 BP;
                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2001; 2001US-00972916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat insulin regulator construct DNA #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABX15373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intestine, to provide insull sections. The prevent diseases associated is useful in gene therapy to treat and/or prevent diseases associated with hyperglycaemia, particularly diabetes, but more generally can be with hyperglycaemia, particularly diabetes, but more generally can be
                                                                                                                                                                                                                                                                                                                                                        (THUL/) THULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intracellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 C;
                                                                                     an insulin regulator construct comprising (GIRE) of a liver pyruvate kinase (LPK) ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
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Pred. No. 4.3
0; Mismatches
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                                                                                                                                                                                                             of insulin
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Query Match
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Matches 51
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The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growth factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-Insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insuliinsulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic; intracellular hormone receptor; insulin regulator construct; anaboli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABX15374;
                                                                                                                                                                                                                                                                                                                                           New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
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                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-674190/72
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                                                                                                                                                                                                                                                     9; Page 14; 37pp;
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Pred. No.
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The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growth factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other

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RESULT 5
ABX15375/c
ID ABX153
XX ABX153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBI insulin-sensitive element; ISE; basal prometer; hyperglycaemia; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatoma; cellular protein degradation; antidiabetic;
                                                                                                                                                                                                                                                                                                                                             New insulin regulator cassette, useful e.g. for provides specific, glucose-inducible transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABX15375
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                                                                                                                                                                                                                                                               Claim 9; Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-OCT-2001; 2001US-00972916.
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                                                                                                                                                                                                                                                                                                                     liver cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 BP; 77 A; 111 C; 84 G; 49 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                   treating diabetes, expression of insulin
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Best Local :
                               to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), tincrease fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other
                                                                                                                                                 The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growth factor binding protein-1 (GFBP-1) basal promoter. The construct is used
                                                                                                                                                                                                                                                                                                               Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                 New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carbohydrates) and glucocorticoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, e.g. inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thule PM;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat insulin regulator construct
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                                                                                                                                                                                                                                                                                                            Page 14; 37pp; English
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Pred. No.
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                                                                                                                                                                                                                                                                                                  exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus; rat; cytosolic pyruvate kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT96631;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat insulin regulator construct of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties
                                                                                        intron
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5917. .6008
'*tag=
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/*tag= k
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6009. .6151
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Pred. No.
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                                Query Match
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Matches 51
                                                                                This DNA encodes a Rattus norvegicus cytosolic pyruvate kinase. The storage lipid content of a seed is increased by reducing the activity endogenous cytosolic pyruvate kinase in the seed. This is applied to plants which accumulate storage procein and lipid in the embryo, particularly an oilseed plant such as soya, sunflower, sesame or especially rapeseed. Inhibitory enzymes involved in amino acid biosynthesis increases production of lipid by directing more of the precursor to the chloroplast
                                                                                                                                                                                                                                                                                                                                                        exon
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                                                                  Sequence 13011
                                                                                                                                                              Claim
                                                                                                                                                                                cytosolic
                                                                                                                                                                                        Increasing
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3021
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51; Conservative
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MITSUBISHI CHEM CORP
               CATGGGCGCACGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 51
CATGGGCGCACGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 3071
                                                                                                                                                              Page 20-25; 28pp; English
                                                                                                                                                                              y storage lipid content pyruvate kinase.
                                                                                                                                                                                                                        Murase J,
                                                                  BP;
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8078. 9297
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7818. .7910

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/number= 9

7911. .8077
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/*tag= u
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/number= 10
9298. .9479
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7302. .74
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RESULT 8

tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising at least part of the data information given in the specification. The methods are useful for predicting at least one toxic effect of a compound, predicting the renal toxicity of a toxic effect of a compound, predicting the renal toxicity of a compound, or identifying toxicity markers in tissues or cells exposed to known renal toxin. The genes are useful as toxicity markers in drug screening and toxicity assays, in monitoring disease physiological states, or disease progression. This polynucleotide represents a rat DNA sequence relating to the toxic effect database

The invention relates to a novel effect of a compound. The method

method of predicting at least one toxic comprises a gene expression profile of a

Of a õ

Example 4; Page; 446pp; English

profile

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a database.

did not

form part

in the specification. NOTE: The sequence data for this orm part of the printed specification, but was obtained c format directly from the World Intellectual Property

patent in

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06-DEC-2001;
19-DEC-2001;
21-FEB-2002;
21-FEB-2002;
21-FEB-2002;
21-FEB-2002;
15-MAR-2002;
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28-AUG-2001;
27-SEP-2001;
27-SCT-2001;
01-NOV-2001;
21-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUN-2001;
10-JUL-2001;
10-JUL-2001;
                                                                                                                                                                                     Predicting at least one toxic effect of a compound, useful for toxicity modeling, comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression
                                                                                                                                                                                                                         WPI; 2003-148464/14.
                                                                                                                                                                                                                                           Mendrick D,
                                                                                                                                                                                                                                                                                                                08-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAY-2001;
13-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         database; drug screening; toxicity assay; rat; ds
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2002US-0372794P.
2002US-0371679P.
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2001US-0303807P.
2001US-0303808P.
2001US-0303810P.
2001US-03034928P.
2001US-0330462P.
2001US-0330462P.
2001US-0331805P.
2001US-0331805P.
2001US-0336144P.
2002US-0357844P.
                                                                                                                                                                                                                                          Porter M,
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2001US-0297523P.
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                                                                                                                                                                                                                                           Castle
                                                                                                                                                                                                                                          ۲
                                                                                                                                                                                                                                           Elashoff M;
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ADP72914
ID ADP7
                                                                         CC The invention relates to a method of predicting (the progression of) a CC toxic effect of a compound by preparing a gene expression profile of a CC kidney tissue or cell sample exposed to the compound and comparing the CC gene expression profile to a database, or detecting the level of gene (s) CC expression in a tissue or cell sample exposed to the compound, where CC differential gene expression). The method is useful for predicting (the progression of) at least one toxic effect of a compound. The genes are CC useful as toxicity progression). The method is useful for predicting (the progression of) at least one toxic effect of a compound. The genes are CC useful as toxicity markers in drug screening and toxicity assays. The CC useful as toxicity markers in drug screening and toxicity assays. The CC useful for predicting the likelihood that a compound or test agent will induce various specific kidney pathologies, such as nephritis, CC kidney necrosis, glomerular and tubular injury, or focal segmental CC glomerulosclerosis. The methods are useful for determining the similarity of a toxic response to one or more individual compounds and for CC predicting or elucidating the potential cellular pathways influenced, CC induced or modulated by the compound or test agent. The kit is useful for predicting the progression of renal disease states, for identifying genes CC that show promise as new drug targets and for screening knew and newly the states of the compound or test compound.
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that show promise as new drug targets and for screening known and newly designed drugs. This sequence corresponds to a gene marker used in the method of the invention. (Note: The sequence data for this patent did no form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Predicting (the progression of) a toxic effect of a compound, for monitoring the progression of renal disease states, comprises preparing a gene expression profile of a kidney tissue or cell sample exposed to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mendrick DL,
Elashoff M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ds; toxic effect; gene expression profile; kidney tissue; differential gene expression; toxicity progression; toxicity marker; drug screening; toxicity assay; kidney pathology; nephritis; kidney necrosis; glomerular injury; tubular injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-460771/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-NOV-2002; 2002US-00301856
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           The invention relates to an insulin regulator construct comprising a CG glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene CC gromoter and an insulin-sensitive element (GSE) of an insulin-like growth CC factor binding protein-1 (IGFBP-1) basal promoter. The construct is used CC to treat or prevent diabetic complications, to regulate insulin CC production, to modulate hyperglycaemia (without severe hypoglycaemia), to CC increase fat catabolism and to retard protein catabolism. The construct CC provides stimulation of insulin expression by glucose (but not other CC carbohydrates) and glucocorticoids and inhibition by glucagon so that a CC combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when CC fed ad libitum and prevent pathological ketogenesis and ketoacidosis, CC thus inhibiting the long-term complications of diabetes. The properties CC of the construct are essentially specific for hepatocytes and well-CC differentiated hepatoma lines and insulin expression in these cells may constitute the construct are essentially specific for hepatocytes and well-CC differentiated hepatoma lines and insulin expression in these cells may constitute the construct are essentially specific for hepatocytes and well-CC differentiated hepatoma lines and insulin expression in these cells may constitute of of other intracellular hormone receptors. This sequence represents a fragment of the rat liver pyruvate kinase glucose response cc element, used in production of the construct of the invention
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Best Local S
Matches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glucose response element; GIRE; liver pyruvate kinase; LPK; 88; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic; intracellular hormone receptor; insulin regulator construct; anabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 10; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-674190/72.
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Pred. No.
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RESULT 11
ABX15380/c
The invention relates to an insulin regulator construct comprising a CC glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene CC promoter and an insulin-sensitive element (ISE) of an insulin-like growth CC factor binding protein-1 (IGPBP-1) basal promoter. The construct is used CC to treat or prevent diabetic complications, to regulate insulin CC production, to modulate hyperglycaemia (without severe hypoglycaemia), to CC increase fat catabolism and to retard protein catabolism. The construct CC provides stimulation of insulin expression by glucose (but not other CC carbohydrates) and glucocorticoids and inhibition by glucagon so that a CC combination of these effects can maintain nearly englycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when CC in diabetics during short-term fasting, large carbohydrate loads or when CC thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-cc differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, e.g. chimbition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a fragment of the rat liver pyruvate kinase glucose response element, used in production of the construct of the invention
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Best Local S
Matches 48
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hepatocyte; hepatoma; cellular protein degradation; antidiabetic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
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Pred. No.
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RESULT 12
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Best Local Similarity
                                                                                                                                  The invention relates to a method of modulation of expression of a DNA molecule (preferably inhibition of lipogenesis or glycolysis) that encodes a protein involved in glucose metabolism or lipogenesis in a cel which comprises contacting the cell with an agent that induces phosphorylation or dephosphorylation of carbohydrate response element binding protein (ChREBP). The method is useful for treating obesity, diabetes or vascular disease and modulating carbohydrate metabolism, for inhibiting lipogenesis or glycolysis and modulating expression of a DNA molecule that encodes a protein involved in glucose metabolism or lipogenesis in a cell (e.g. human liver cell) and for treating cardiac disease. The present sequence represents an oligonucleotide used in the purification of ChREBP
                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                             Modulation of the expression of DNA molecule that encodes involves use of an agent that induces phosphorylation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ss; lipogenesis; glycolysis; glucose metabolism; carbohydrate response element binding protein; ChREBP; obesity; diabetes; vascular disease; carbohydrate metabolism; cardiac disease.
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                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 2;
                                                                                                                                                                                                                                                                                                                                                dephosphorylation of
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                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA
                           CATGGGCGCACGGGCACTCCCGTGGTTCC
                                                                                                            30 BP; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGCGCACGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                           A; 11 C; 11 G; 5 T; 0
                                                 58.8%; UT
100.0%; Pr
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.1%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                carbohydrate response
                                                                                                                                                                                                                                                                                                                     64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30
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                                                                    Score 30;
Pred. No.
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Pred. No.
                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6; 1
                                                                                 DB 12;
30
                                                                    0.65;
                                                                                                           U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                element binding
                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 51
                                                                               Length 30;
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                       Gaps
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                                                       0
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RESULT 13 ADE83567/c

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RESULT 14
ADE83566
ID ADE83
XX ADE83
XX ADE83
XX ADE83
XX L-Dy1
XX L-Dy1
XX Ads; 1
XX Ads; 1
XX Cascu
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                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                          molecule (preferably inhibition of lipogenesis or glycolysis) that encodes a protein involved in glucose metabolism or lipogenesis in a cell which comprises contacting the cell with an agent that induces phosphorylation or dephosphorylation of carbohydrate response element binding protein (Chribb). The method is useful for treating obesity, diabetes or vascular disease and modulating carbohydrate metabolism, for inhibiting lipogenesis or glycolysis and modulating expression of a DNA molecule that encodes a protein involved in glucose metabolism or lipogenesis in a cell (e.g. human liver cell) and for treating cardiac disease. The present sequence represents a L-pyruvate kinase carbohydrate response element.
           ds; lipogenesis; glycolysis; glucose metabolism;
carbohydrate response element binding protein; ChREBP; obesity; diabetes;
vascular disease; carbohydrate metabolism; cardiac disease;
                                                                    L-pyruvate kinase carbohydrate response element
                                                                                                                              ADE83566;
                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulation of the expression of DNA molecule that encodes protein involves use of an agent that induces phosphorylation or dephosphorylation of carbohydrate response element binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ds; lipogenesis; glycolysis; glucose metabolism;
carbohydrate response element binding protein; ChREBP; obesity; diabetes;
vascular disease; carbohydrate metabolism; cardiac disease;
                                                                                                                                                         ADE83566 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; SEQ ID NO 4; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-020312/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Uyeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001; 2001US-0329834P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2003124590-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L-pyruvate kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2002; 2002US-00272206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L-pyruvate kinase carbohydrate response element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADE83567 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYED/)
                                                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                                       27;
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                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                               GGGCGCACGGGGCACTCCCGTGGTTCC 1
                                                                                                                                                                                                                                                         GGGCGCACGGGGCACTCCCGTGGTTCC 30
                                                                                                                                                                                                                                                                                                                                                 27
                                                                                                                                                                                                                                                                                                                                              BP; 4 A;
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                 52.9%;
                                                                                                                                                                                                                                                                                                                                               11 C;
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                                                                                                                                                                                                                                                                                                  Score 27;
Pred. No.
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                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                            2 T; 0 U;
                                                                                                                                                                                                                                                                                                    DВ
7;
                                                                                                                                                                                                                                                                                                                12; Length 27;
                                                                                                                                                                                                                                                                                                                                              0 Other;
                                                                                                                                                                                                                                                                                     0,
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                                                                                                                                                                                                                                                                                    0;
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RESULT 15
ADE83614
ID ADE83
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Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of modulation of expression of a DNA molecule (preferably inhibition of lipogenesis or glycolysis) that encodes a protein involved in glucose metabolism or lipogenesis in a ce which comprises contacting the cell with an agent that induces phosphorylation or dephosphorylation of carbohydrate response element binding protein (Chreap). The method is useful for treating obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetes or vascular disease and modulating carbohydrate metabolism, for inhibiting lipogenesis or glycolysis and modulating expression of a DNA molecule that encodes a protein involved in glucose metabolism or lipogenesis in a cell (e.g. human liver cell) and for treating cardiac disease. The present sequence represents a L-pyruvate kinase carbohydrate
                                                                                                                                                          carbohydrate response element binding protein; ChREBP; obesity; diabetes; vascular disease; carbohydrate metabolism; cardiac disease; gel shift assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modulation of the expression of DNA molecule that encodes protein involves use of an agent that induces phosphorylation or dephosphorylation of carbohydrate response element binding protein
                                                                                                                                    Unidentified
                                                                                                                                                                                                  ss; lipogenesis; glycolysis; glucose metabolism;
                                                                                                                                                                                                                             ChREBP gel shift assay gene sequence
                                                                                                                                                                                                                                                           29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                        16-OCT-2001; 2001US-0329834P
                                                    16-OCT-2002; 2002US-00272206
                                                                                                         US2003124590-A1
                                                                                                                                                                                                                                                                                                              ADE83614 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-020312/02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUL-2003
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(UYED/) UYEDA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2002; 2002US-00272206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     element.
                                                                                                                                                                                                                                                                                                                                                                                  GGGCGCACGGGGCACTCCCGTGGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 BP; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                      52.9%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                #1
                                                                                                                                                                                                                                                                                                                                                                                                           30
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7;
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Search completed: September 1, 2005, 00:34:35 Job time: 60.0797 secs
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                                                                                                                                                                    Query Match 51.0%; Score 26; DB Best Local Similarity 100.0%; Pred. No. 15; Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                  The invention relates to a method of modulation of expression of a DNA molecule (preferably inhibition of lipogenesis or glycolygis) that encodes a protein involved in glucose metabolism or lipogenesis in a cell which comprises contacting the cell with an agent that induces phosphorylation or dephosphorylation of carbohydrate response element binding protein (ChREBP). The method is useful for treating obesity, diabetes or vascular disease and modulating carbohydrate metabolism, for inhibiting lipogenesis or glycolysis and modulating expression of a DNA molecule that encodes a protein involved in glucose metabolism or lipogenesis in a cell (e.g. human liver cell) and for treating cardiac disease. The present sequence represents a ChREBP gel shift assay gene
                                                                                                                                                                                                                                                            Sequence 26 BP; 2 A; 9 C; 11 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 14; SEQ ID NO 51; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modulation of the expression of DNA molecule that encodes protein involves use of an agent that induces phosphorylation or dephosphorylation of carbohydrate response element binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-020312/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Uyeda K;
                                                                                   GGGCGCACGGGGCACTCCCGTGGTTC 29
                                                                                                                                                                                             DB 12; Length 26; 15;
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Run
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seg length: 0
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Gapop 10.0 , Gapext 1.0
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2248.600 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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372
372
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  US-09-972-916A-1

US-09-972-916A-3

US-09-972-916A-5

US-09-972-916A-5

US-09-972-916A-6

US-09-972-916A-6

US-10-388-934-36

US-10-152-319A-2150
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                                                                                                                                                                                                                                                               SUMMARIES
Sequence 1, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 36, Appl
Sequence 2150, Ap
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46.7	46.7	•	•	•	•	47.1	•	•	47.1	47.1	47.1		47.1	•	•	•	•	•		٠	47.1	•	٠	٠	٠	٠	•								52.9		71.8
27	27	27	27	2046	2046	2046	2046	2046	2046	2046	2046	1905	1595	1579	1546	1498	1333	1311	1191	1188	1188	525	209	3511	3138	3138	3138	3138	3138	10	55001	10	26	27	27	30	31703
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US-10-272-206-8	-10-272-206	-10-272-206	-10-272	-10-103	-10-073-	764	-09-764-	US-09-989-442-155	US-09-764-853-875	US-09-764-886-84	US-09-764-893-130	US-10-505-486-226	US-09-798-710-1	885-1	US-10-225-567A-584	9-826-508-3		-10-029-	US-10-343-650A-45	11-086-846-	US-10-094-417-3	US-10-029-386-12527	US-10-029-386-26227	US-10-723-860-4919	US-10-756-149-213	US-10-723-860-176	US-10-342-887-909	US-10-172-118-909	09-880-107-171	-10-991-1	-10-348-750-	-10-160-497-	-10-272-206-	-10-272-206-	-10-272-206-	-10-272-206-	US-10-085-117-172
Sequence 8, Appli		о С	O	592	e 13(1209	84	155,	Sequence 875, App	84, 1	w	e 23	ς.	11,	e 58	w	19		45	ω	3, Appl	129	26227,	4919,		176,	909,	e 909,	1716, Ap	Α.		4	51,	4	e 3,		Sequence 172, App

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US-09-972-916A-1
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                                                                                                                                                                                                                         Sequence 1, Application US/09972916A
Patent No. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thile, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1992/01 (VA)
CURRENT APPLICATION UNMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 1
                                                                                   Query Match
Best Local S
                                                                   Matches
                                                                                                                                                          TYPE: DNA
ORGANISM: Rattus
FEATURE:
                                                                                                                                                                                                              LENGTH: 51
                                                                                 Local
                               1 CATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 51
                                                                                     Similarity
CATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 51
                                                                   100.0%;
ilarity 100.0%;
Conservative 0
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                                                                   Score 51; DB 9; 1
Pred. No. 8.1e-09;
0; Mismatches 0;
                                                                                                    Length 51;
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RESULT 2

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Best Local S
Matches 51
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APPLICANT: Thule, Peter M.
APPLICANT: Thule, GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 4
SEQ ID NO 5
         APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
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Best Local Similarity
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TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthesized -09-972-916A-4
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PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Thule, Peter M.

APPLICANT: Thule, CLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION

FILE REFERENCE: US 1292/01 (VA)

CURRENT APPLICATION NUMBER: US/09/972,916A

CURRENT FILING DATE: 2001-0-10

PRIOR APPLICATION NUMBER: US 60/239,113

PRIOR FILING DATE: 2000-10-11
                                                                                                                                                                       SOFTWARE: PatentIn version 3.1 SEQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 6
SEQ ID NO 6
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Patent No. US20020107198A1
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Best Local Similarity
                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 02005336.9 PRIOR FILING DATE: 2002-03-14 PRIOR APPLICATION NUMBER: 02015657.6 PRIOR FILING DATE: 2002-07-17 NUMBER OF SEQ ID NOS: 862
                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Boess, Franziska
APPLICANT: Suter-Dick, Lau
                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
                                                                                                           LENGTH: 13011
TYPE: DNA
ORGANISM: Rattus
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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Wolf, Detlef
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ilarity 100.0%;
Conservative 0
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                 Score 51; DB 17;
Pred. No. 3.2e-09;
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Pred. No. 5.8e-09;
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                                                     Length 13011;
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PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR FILING DATE: 2001-07-10
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Best Local S
Matches 51
                                                                                                                                                                Sequence 172, Application US/10085117 Publication No. US20030232334A1 GENERAL INFORMATION:
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SEQ ID NO 2150
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          APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: 529452000121
CURRENT APPLICATION NUMBER: US/10/085,117
CURRENT FILING DATE: 2002-02-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 2221
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PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Genbank Accession No. X05684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/303,808 FILING DATE: 2001-07-10 APPLICATION NUMBER: US 60/315,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/330,867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2001-08-28
                                                                                                                                                                                                                                                                                                                                      3021 CATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 307
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Higgs, Brandon
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 51; DB 18; 100.0%; Pred. No. 3.2e-09;
US 09/798,586
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                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 13011;
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RESULT 10 US-10-272-206-3

Sequence 3, Application US/10272206 Publication No. US20030124590A1

GENERAL INFORMATION:
APPLICANT: KOSAKU UYOEdA
TITLE OF INVENTION: CARBOHYDRATE RESPONSE ELEMENT BINDING
TITLE OF INVENTION: PROTEIN AND USES THEREOF
TILE OF INVENTION: PROTEIN AND USES THEREOF
FILE REFERENCE: A34675 090495.0240
CURRENT FILING DATE: 2002-10-16
CURRENT FILING DATE: 2001-10-16
PRIOR PELLING DATE: 2001-10-16
PRIOR PILING DATE: 2001-10-16

SOFTWARE: SEQ ID NO 3

ORGANISM: Artificial Sequence

TYPE: DNA LENGTH: NUMBER OF SEQ ID NOS: 66

FastSEQ for Windows Version 4.0

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                                                                                                                                                 US-10-272-206-2
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US-10-272-206-2
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                                                                                                                                                                                                                                       SEQ ID NO 2
LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10272206
Publication No. US20030124590A1
GENERAL INFORMATION:
APPLICANT: Kosaku Uyeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 172
                                                                          Matches
                                                                                           Best Local Similarity
                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: CARBOHYDRATE RESPONSE ELEMENT BINDING TITLE OF INVENTION: PROTEIN AND USES THEREOF FILE REFERENCE: A34675 900495.0240
CURRENT APPLICATION NUMBER: US/10/272,206
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 60/329,834
PRIOR FILING DATE: 2001-10-16
                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: variation
LOCATION: (1)...(31703)
OTHER INFORMATION: n = any nucleotide
                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Oligonucleotide
                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 31703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.8%;
Local Similarity 90.7%;
es 39; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2120
                                                                        30;
                                    1 CATGGGCGCACGGGGCACTCCCGTGGTTCC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCCAGTGTA 51
CATGGGCGCACGGGGCACTCCCGTGGTTCC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCTGGCATA 2078
                                                                        Conservative
                                                                                         100.0%;
                                                                                       58.8%; Score 30; DB 15; 100.0%; Pred. No. 0.31;
                                                                        <u>,</u>
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                                                                        Mismatches
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                                                                        0
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RESULT 12
US-10-272-206-51
; Sequence 51, Application US/102
; Publication No. US20030124590A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: CARBOHYDRATE RESPONSE ELEMENT BINDING TITLE OF INVENTION: PROTEIN AND USES THEREOF FILE REFERENCE: A34675 090495.0240
CURRENT APPLICATION NUMBER: US/10/272,206
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 60/329,834
PRIOR FILING DATE: 2001-10-16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 27
TYPE: NA
                                                                                                                         SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 26
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: KOSAKU UYOGA
TITLE OF INVENTION: CARBOHYDRATE RESPONSE ELEMENT BINDING
TITLE OF INVENTION: PROTEIN AND USES THEREOF
FILE REFERENCE: A34675 090495.0240
CURRENT APPLICATION NUMBER: US/10/272, 206
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 60/329,834
PRIOR FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 66
                     Query Match
Best Local
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APPLICANT: Kosaku Uyeda
   Matches
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Publication No. US20030124590A1
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Best Local :
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                          OTHER INFORMATION:
                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Oligonucleotide from wild type pyruvate kinase OTHER INFORMATION: carbohydrate response element (ChRE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Oligonucleotide from wild type pyruvate kinase OTHER INFORMATION: carbohydrate response element (ChRE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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 l Similarity
26; Conserv
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27; Conserv
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51.0%; Score 26; DB llarity 100.0%; Pred. No. 8. Conservative 0; Mismatches
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                                                                                          Oligonucleotide
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100.0%; Pr/
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100.0%; Pred. No. 3.8;
tive 0; Mismatches 0
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                 DB 15;
. 8.7;
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                                    Length 26;
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RESULT 15 US-10-991-147-4

Sequence 4, Application US/10991147
Publication No. US20050096292A1
GENERAL INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: Kenneth W. Dobie

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US-10-348-750-4
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US-10-160-497-4
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10348750 Publication No. US20030225019A1 GENERAL INFORMATION:
                                                                                                                                                                                                                       SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: Kenneth W. Dobie
APPLICANT: Erich Koller
TITLE OF INVENTION: ANTISENSE MODULATION OF NOTCH1 EXPRESSION
                                                               Best Local Similarity Matches 33; Conserv
                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                     TITLE OF INVENTION: NOTCH1 INHIBITORS FOR INDUCING APOPTOSIS FILE REFERENCE: ISPH-0729
CURRENT APPLICATION NUMBER: US/10/348,750
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: 10/160,497
PRIOR PILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 146
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Susan M. Freier
APPLICANT: Kenneth W. Dobie
APPLICANT: Erich Koller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/160,497
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: RTS-0386
                                                                                                                                                     FEATURE:
                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 55001
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                     LENGTH: 55001
27032 GGGTCCACGGGCTCTCGCTGGCTTCCCGCCCTCTCCCCACTGTGT 27078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27032 GGGTCCACGGGCTCTCGCTGGCTTCCCGCCCCCCCCCACTGTGT 27078
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                               GGGCGCACGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGT
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                                                                 Conservative
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                                                                                 48.2%;
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                                                                 0,
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                                                                                 Score 24.6;
Pred. No. 7.
                                                                   Mismatches
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5
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                                                                   Indels
                                                                                                 Length 55001;
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APPLICANT: Erich Koller
ITITLE OF INVENTION: NOTCH1 INHIBITORS FOR INDUCING APOPTOSIS
PILE REFERENCE: ISPH-0729
CURRENT EPILICATION NUMBER: US/10/991,147
CURRENT FILING DATE: 2004-11-17
PRIOR APPLICATION NUMBER: US/10/348,750
PRIOR PILING DATE: 2004-01-21
PRIOR PILING DATE: 2003-01-21
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM nucleic - nucleic search, using sw model
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length: 2000000000
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Match Length DB
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  97.0
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(c) 1993 - 2005
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AC136382
MMILGF
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7782.159 Million cell updates/sec
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Compugen Ltd.
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                                                                             AX401932 Sequence
AX827271 Sequence
M58634 Rat IGF bin
AX163782 Sequence
L22979 Rat insulin
                           AY095345 Papio anu
G67139 IGFBP1 X1.1
AX409747 Sequence
M74587 Human insul
                                                                                                                         AC136382 Rattus no
X67493 M.musculus
AL607124 Mouse DNA
BC013345 Mus muscu
M59316 Human insul
AY434089 Homo sapi
                                                                                                                                                                               Description
                 174587 Human insul
G19994 sWSS752 Eri
                                                            AY560836 Spermophi
BC078889 Rattus no
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ALIGNMENTS

REFERENCE AUTHORS JOURNAL COMMENT SOURCE ORGANISM RESULT 1
RATILGFZ
LOCUS
DEFINITION
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KEYWORDS ORIGIN FEATURES source Unterman,T.G., Lacson,R.G., McGary,E., Whalen,C. and Goswami,R. Biochem. Biophys. Res. Commun. (1991) In press Original source text: Rattus norvegicus (strain Sprague-Dawley) male adult liver DNA. M84484.1 GI:204927 insulin-like growth factor. Rattus norvegicus (Norway rat) Rattus norvegicus insulin-like ç M84484 Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. (bases 1 to 1181) /tissue_type="liver" /dev_stage="adult" /organism="Rattus norvegicus" /mol_type="genomic DNA" /strain="Sprague-Dawley" /db_xref="taxon:10116" Location/Qualifiers sex="male" . .1181 p DNA linear ROD 27-growth facter gene fragment. and Goswami, R.G ROD 27-APR-1993

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Best Local Similarity 99.5 Matches 213; Conservative

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Score 212.4; DB 1 Pred. No. 2.2e-53; 0; Mismatches 1

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 Rat Genome Sequencing Consortium
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9, *** SEQUENCING IN PROGRESS
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 135613 bases at least Q30
Consensus quality: 140849 bases at least Q30
Consensus quality: 145680 bases at least Q20
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Center clone name: CH230-97018
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Contact: hgsc-help@bcm.tmc.edu
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X67493
X67493.1 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-JUL-1992) R.A. Taub, Univ. of Pennsylvania, Hughes Medical Institute, Clinical Research Bldg., Room 4: Curie Boulevard, Philadelphia, PA 19104-6145, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 1363)
Mohn, K.L., Waddle, J.R. and Taub, R.
Comparison of mouse and human IGFB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mohn,K.L., Bucan,M. and Taub,R. Structure and localization of the IGFBP-1 gene and its expression during liver regeneration Hepatology 19 (3), 656-665 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1363)
Lee,J., Greenbaum,L., Haber,B.A., Nagle,D., Lee,V., Miles,V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insulin-like growth Mus musculus (house
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 1363)
                                                                                                                                                                                                                                                                                                         /cell_line="NIH 3T3"
/cell_type="fibroblast"
/clone_lib="genomic, lamt
/dev_stage="embryo"
500 _ sca
                                                                                                                                                               sequences"
764. .768
792. .1336
                                                                                                                                                                                                                                                                                                  500.
            /codon_start=1
/product="insulin-like growth
/protein_id="CAA47832.1"
/db_xref="GI:52700"
/db_xref="GOA:P47876"
                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
/mol_type="genomic DNA"
/strain="NIH Swiss"
                                                                                                               note="mRNA
                                                                                                                                                  'number=1
                                                                                                                                                                                                                 note="Caat
                                                                                                                                                                                                                                                                               note="AP-2
                                                                                                                                                                                                                                                                                                                                                                               clone="JW2.1"
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db_xref="UniProt/Swiss-Prot:P47876"
                                                                                                                                                                                                                                                note="insulin-responsive element"
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                                                                                                                 cap site"
                                                                                                                                                                                                                                                                                 consensus
                                                                                                                                                                                                                 box with APF, HNF and NF-E1
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                                                                                                                                                                                                                                                                                                                               lambda
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                                                                 factor binding protein-1"
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Room 475, 422
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Best Local
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                                                                                 source
                                                                                                                                                                                                                                                           AL Submitted (11-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
    humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
    On Apr 12, 2002 this sequence version replaced gi:19847866.
    During sequence assembly data is compared from overlapping clones.
    Where differences are found these are annotated as variations
    together with a note of the overlapping clone name. Note that the
    variation annotation may not be found in the sequence submission
    corresponding to the overlapping clone, as we submit sequences with
    only a small overlap as described above.
    This sequence was finished as follows unless otherwise noted: all
    regions were either double-stranded or sequenced with an alternate
    chemistry or covered by high quality data (i.e., phred quality >=
    30); an attempt was made to resolve all sequencing problems, such
    as compressions and repeats; all regions were covered by at least
    one plasmid subclone or more than one Ml3 subclone; and the
    assembly was confirmed by restriction digest. The following
    abbreviations are used to associate primary accession numbers given
    in the feature table with their source databases: Em:, EMBL; Sw:,
    SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
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                                                                                                                                                   constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpepfrom the RPCI-23 Mouse PAC Library
                                                                                                                                                                                                                                                    database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/organism="Mus musculus
/mol_type="genomic DNA"
/db_xref="taxon:1000"
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Pred. No. 4.1e-46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                    Submitted (31-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC013345 1569 bp mRNA linear ROD Mus musculus insulin-like growth factor binding protein (cDNA clone MGC:14075 IMAGE:4161889), complete cds.
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                                                                                                    Contact: MGC help desk
                                                                                                                      NIH-MGC Project URL: http://mgc
                                                                                                                                                                                                                                               Direct Submission
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/clone_lib="RPCI-23"
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Pred. No. 4.
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Best Local Similarity 92.8
Matches 103; Conservative
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Series: IRAK Plate: 18 Row: i Column: 20
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                       Mendrick, D.,
Blashoff, M.R.
                                                                                                                                                                                                                                                      Rattus norvegicus (Norway rat)
   Molecular toxicology modeling Patent: WO 0210453-A 1608 07-FEB-2002;
                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Codon_start=1
/product="insulin-like growth factor binding protein 1"
/protein id="AAH13345.1"
/protein id="AAH13345.1"
/db_xref="GI:15426483"
/db_xref="MGI:96496"
/db_xref="MG
                                                                                                                                                                                                                                                                                                                                                                                                                 1608 from Patent
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/db_xref="LocusID:16006"
/db_xref="MGI:96436"
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/clone="MGC:14075 IMAGE:4161889"
/tissue_type="Liver; normal. 5 mv
/clone_Tib="NCI_CCAP_Li9"
/lab_host="DH10B"
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|strain="FVB/N"
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                                                                                            Porter, M.W.,
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92.8%;
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t WO0210453
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                                                                                            Johnson, K.R.,
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                                                                                                  Castle, A.L.
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                                                        N Rat IGF binding protein-1 (rIGFBP-1) mR 4 M58634 m58634.1 GI:204732 IGF binding protein-1. Rattus norvegicus (Norway rat) M Rattus norvegicus Eukarvers Mr.
                                                                                                                                                                                                                                 197 CACTTCCGCTACTAGCTA 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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AX827271
Mohn, K.L., Melby, A.E.,
                          Rattus.
                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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              (bases 1 to 1500)
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                                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
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/mol type="unassigned DNA"
/mb type="taxon:10116"
/noTe="EMBL/GenBank Accession
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98.7%;
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                                       Chordata;
Rodentia;
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Pred. No. 3.7e.
0; Mismatches
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Pred. No. 3.7e-1
0; Mismatches
Tewari, D.S.,
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                                       Craniata; Vertebrata; |
Sciurognathi; Muridae;
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3.7e-12;
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Laz,T.M.
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                                                     Euteleostomi;
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                                          Murinae;
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Curagen
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Sequence 46
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AX163782.1
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is rapidl
Mol. Cell
91141487
                                                                                                                                                                                           Gould-Rothberg, B.E., Dipippo, V.A., Ramseh, T.M. and Gerwein, R.W. Method of identifying toxic agents using nsaid-induced differential gene expression in liver
                                                                                                                                                                                                                                                                                    Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                       Similarity
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CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e gene encoding rat insulinlike growth factor-binding protein rapidly and highly induced in regenerating liver
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                      WO 0138579-A 46 31-MAY-2001;
Corporation (US)
                                                                                                     /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNKNGFYHSKQCETSLDGEAGLCWCVYPWSGKKIPGSLETRGDPNCHQYFNVQN"
                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="IGF binding protein-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="IGF binding protein-1"
/protein_id="AAA41380.1"
/db_xref="GI:204733"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="regenerating liver"
/dev_stage="adult"
.co__ara
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Patent WO0138579
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                                      Score 76.4; DB 6;
Pred. No. 3.7e-12;
0: Mismatches 1;
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No. 3.7e-12;
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Lacson, R., Oehler, D.,
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               4090.
   number=4
                         number=3
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                                                                                                                                                                                                                                                                                                                                                                                                                            tissue
                                                                                                     number=2
                                                                                                                                             number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="male"
                                                                                                                                                                                  number=1
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Lacson,R., Oehler,D., Yang,E., Goswami,R. and Unterman,T. Dideoxy sequencing and structural analysis of the rat ins growth factor binding protein-1 gene Biochim. Biophys. Acta 1218 (1), 95-98 (1994)
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Original source text: Rattus norvegicus (strain Sprague-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RATIGFBA 5001 bp UNA LINGAL NO TO THE RATIGEBA (IGFBP-1) gene, Rat insulin-like growth factor binding protein-1 (IGFBP-1) gene,
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QGACVLEPAAPATSSLSGSQHEEAKAAVASEDELAESPEMTEEQLLDSFHLMAPSRED
QPILMNAISTYSSMRAREITDLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
                                                                                                                                                                                                                                                                                                                                                                                   CNKNGFYHSKQCETSLDGEAGLCWCVYPWSGKKIPGSLETRGDPNCHQYFNVQN"
gene="IGFBP-1"
                                                                               9874. .3002
|
| gene="IGFBP-1"
                                                                                                                                                                 2035. .2873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="insulin-like growth factor binding protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(153. .525,1850.
/gene="IGFBP-1"
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/db_xref="taxon:10116"
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gene="IGFBP-1"
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                                                                                                                                                                                                                                                                                                                                   gene="IGFBP-1"
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
TITLE
                                                                                                                                                                        Query Match
Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
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Best Local :
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431
                                              491 TAACTTTCTAGTCCAAGTGGAGTGAACCGCGCCCTTTATAAGGCAAGGGCTGCACCCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1507)
Li,Y., Klimanis,D. and Hallenbeck,J.M.
Cloning and characterization of insulin-like
protein 1 (IGFBP-1) from thirtean-lined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermophilus tridecemlineatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AY560836 1507 bp mRNA Spermophilus tridecemlineatus insulin-like Spertein 1 (IGFBP1) mRNA, complete cds.
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77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (27-FEB-2004) StrokeBranch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spermophilus
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                                                                                                          CAGGAGCAAAACATATTTTTGAACACTGGGCTCCTAGCACGCCGCGCTGGCAATCAT
                                                                                                                                          CACAAGCAAAACATATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCAT
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                                                                                                                                                                                                                                                            /protein_id="AAS67029.1"
/db_xref="GI:45505309"
/translation="MPEVPAAGLMPFLLLLAVQVSTVASSTQPWHCAPCSAEKLALCP
/translation="MPEVPAAGLMPFLLLLAVQVSTVASSTQPWHCAPCSAEKLALCP
PVESSCPELSRPAGCCCCPMCALPLGAACGVATARYARGLSCRALPGEPRPHALTRG
GGACVPEPATPTASGLSSIEKEEAKASMVPERVPPESAEMTEEQLLESFHLMASSSED
QPILMNAISTYKSMRAREMAIIKKMKQPCRRELYKVLERLAKAQQKAGEEIYKFYLPN
                                                                                                                                                                                                                                                   CNKNGFYHSKQCETSLDGEAELCWCVYPWSGRRIPGSLEIRGDPNCHQYFNVQN"
                                                                                                                                                                                                                                                                                                                                         /product="insulin-like growth factor binding protein
/protein_id="AAS67029.1"
                                                                                                                                                                                                                                                                                                                                                                                           /gene="IGFBP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="IGFBP1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Spermophilus
                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
                                                                                                                                                                                    34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       xref="taxon:43179"
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                                                                             -GTGCTGCCGAGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAGC 111
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Pred. No. 3.7e-12;
                                                                                                                                                                                      Score 76.2; DB 10;
Pred. No. 4.2e-12;
                                                                                                                                                                         Mismatches
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AUTHORS
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BC078889
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                                              source
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RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Razywinski, M.I., Skalska, U., Smailus, D.E.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   551 AAGCATCGTGCACTGCCCACGGCGACTCAGAATTGGACACCTATCAA-----GCCACTGC 605
                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 184 Row: e Column: 23
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-AUG-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@pasxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Howard Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway rat)
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                                                                                                                                                                              passed the following selection criteria: matched mRNA gi: 6981079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
                                                                                                                                             Location/Qualifiers
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REFERENCE
AUTHORS
TITLE
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ORGANISM
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AY095345
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VERSION
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Best Local S
Matches 66
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                                                                                                                                                                                                                           i (bases 1 to 3886)
Kim, J.J., Taylor, H.S., Akbas, G.E., Foucher, I., Trembleau, A.,
Jaffe, R.C., Fazleabas, A.T. and Unterman, T.G.
Regulation of insulin-like growth factor binding protein-1 promoter activity by FKHR and HOXA10 in primate endometrial cells
Biol. Reprod. 68 (1), 24-30 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               μ
                                                                                                                            Submitted (11-APR-2002) Department of Obstetrics and Gynecology, University of Illinois at Chicago, 820 S. Wood, Chicago, IL 60612,
                                                                                                                                                                            2 (bases 1 to 3886)
Kim, J.J., Jaffe, R.C.
                                                                                                                  USA
                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithe
                                                                                                                                                                                                                                                                                                                                                                                                                               AY095345.1 GI:20853764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AY095345
Papio anubis insulin-like growth factor binding protein-1
                                                                                                                                                                                                                                                                                                                              Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                Papio anubis
                                                                                                                                                                                                                                                                                                                                                                                               Papio anubis (olive baboon)
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        /mol_type="ye..........9555"
/db_xref="taxon:9555"
<3655. .>3886_...
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QPILMNAISTYSSMRAREITDLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="insulin-like growth factor binding protein
/protein_id="AAH78889.1"
/db_xref="GI:50927647"
/gene="IGFBP-1"
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                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="MGC:33595 IMAGE:7129185"
/tlssue_type="Kidney, rat (Brown
/clone_lib="NNH_MGC_236"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="LocusID:25685"
/db_xref="RATMAP:44422"
/db_xref="RGD:2872"
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/db_xref="LocusID:25685"
/db_xref="RATMAP:44422"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Igfbp1"
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Pred. No. 7.9e-09;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                               Cercopithecidae;
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G67139
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STS.
                                                                Buffer:
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                              MgCl2:
KCl:
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Query Match
Best Local Similarity
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International Agency for Research
150, cours Albert-Thomas, F-69372
Tel: +33-4-72738698
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 448)
Cox,D.G., Boillot,C. and Canzi Genome Survey
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                                                                                                                                                                                                            STS size: 448
                                                                                                                                                                                                                                                            Email: canzian@iarc.fr
                                                                                                                                                                                                                                                                              Fax: +33-4-72738388
                                                                                                                                                                                                                                                                                                                                                             Contact: Federico Canzian
                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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Primer:
dNPTs:
MgCl2:
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/codon_start=1.
/codon_start=1.
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/translation="WSEPVARVWLVLLLLTYQVGVTASAPWQCAPCSAEKLALCPPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="IGFBP-1"
/product="insulin-like
3655. .>3886
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GGGTGACCTCCGAGCACG
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Pred. No. 5.7e-08;
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RESULT 15
AX409747
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DEFINITION
ACCESSION
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VERSION
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source
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Best Local Similarity 66.5
Matches 141; Conservative
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Best Local Similarity 66.5
Matches 141; Conservative
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                                                                                                                                                                    473 CACTAGCAAAACATATTTTGAACACTCAGCTCCTAGCGTGCGGCGCTGCCAATCAT
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171
                                593
                                                            112 CAGCATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGC-ACACGG 170
                                                                                                  533 TAACCTCCTGGTGCAAGTGGCGCGGCCTGTGCCCCTTTATAAGGTGCGCGCTGTGTCCAGC
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                                                                                                                                                                                                                                                                                                                                                                                            Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G. Gene expression profiles in liver cancer patent: WO 0229103-A 2394 11-APR-2002; GENE LOGIC INC (US)
Location/Qualifiers
1. .6128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 2394 from Patent WO0229103.
AX409747 GI:21442452
CCATCTGCCCAGAGAGCTGTGACCACCACTTC 202
                                 GAGCATCGGCCACCGCCATCC-----CATCCAGCGAGCATCTGCCGCCGCCGCCGCCG
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                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/noCe="EMBL/GenBank Accession No. M74587"
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/clone_lib="Human"
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66.5%;
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Pred. No. 1.9e-07;
0; Mismatches 52;
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645 CACCCTCCCAGAGAGCACTGGCCACCGCTCC 676

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Search completed: September 1, 2005, 03:26:45 Job time : 1371.59 secs This Page Blank (uspto)

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34239544 segs, 19032134700 residues
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gb_ntc::
gb_htc::
gb_est3::
gb_est4::
gb_est5::
gb_est5::
gb_est6::
                                                                                                                                                                                                                                Length DB
GenCore version (c) 1993 - 2005
                                  A1528304
A1196154
A1785039
CO573026
CV127049
CO560662
CV575629
CV117001
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BY783538
BY794229
BY771317
AI785818
AI196314
AI530146
                 BB660958
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Compugen Ltd.
                        CV127049 AGENCOURT
CO560662 AGENCOURT
CO575629 AGENCOURT
CV117001 AGENCOURT
W30013 mc24c07.r1
                                                                             AI529939 ui87c09.y
CA478518 AGENCOURT
AI790802 uk28b10.y
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AI785039 ui73a06.y
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AI530146 ui89f09.y
AI098594 ue31e07.y
AI530313 ui91f01.y
                 W30013 mc24c07.rl
BB660958 BB660958
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35	35	35	35	35	35	35	35	35	36.8	36.8	38.8	59	60.8	60.8	61.6	61.8	62.8	64.4	65.4	67.4
16.0	16.0	16.0	16.0	16.0	16.0	16.0	16.0	16.0		16.8	17.7	26.9	27.8			28.2	28.7	29.4	29.9	30.8
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AA133272	BM765253	BX371876	BM772026	BG388790	BG283072	AA443181	BX282084	Т87256 у	AL208895	BF829782	BU684425	AA060360	CR595377	CR621807	AW916227	BB604790	AA105355	CK473709	CK472246	AA674302
zl16h11.	K-EST0046	BX371876	K-EST0056	602414492	602406695	zx98h10.r	BX282084	87256 yd91c06.rl	Tetraodon	MR3-HN006	UI-CF-ENO	mj67a12.r	full-leng	full-leng	EST347531	BB604790	mp37d09.x	AGENCOURT	AGENCOUR1	vp96g10.1

ALIGNMENTS

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REFERENCE
AUTHORS
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VERSION
KEYWORDS
SOURCE
ORGANISM
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BF236974
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Query Match
Best Local Similarity
Matches 103; Conserv
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1013)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM9443 row: j column: 02 High quality sequence stop: 581. Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                        /db_xref="taxon:10090"
/clone="IMAGE:416:1889"
/lab host="PH108 (T1 phage-resistant)"
/clone_lib="NCI CGAP_Li9"
/clone_sib="NCI CGAP_Li9"
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: Not Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP_Library."
                                                                                                                                                                                                                                                                                                    mol_type="mRNA"
strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
                     44.8%;
92.8%;
Score 98.2; DB 2;
Pred. No. 1.2e-18;
0; Mismatches 8;
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104 TGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTG 163

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BY783538.1
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please visit our web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY783538 RIKEN full-length enriched, 17.5 days embryo Mus musculus cDNA clone L930176D05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 310)
Carninci, P., Waki, K., Shiraki, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                              Similarity
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TGCCCAGAGAGCTGTGACCACCACCTTCCGCTACTAGCTA 214
                                                                                   ATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATC
                                                            ATGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACACGGCCGTCTGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 119
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                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   visit our web site (http://genome.gsc.riken.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                      /tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5
                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="L930176D05"
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                                                                                                                                                              40.1%;
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                                                                                                                                                            Score 87.8; DB 6;
Pred. No. 1.3e-15;
                                                                                                                                           Mismatches
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Sciurognathi; Muridae; Murinae;
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d, 17.5 days embryo whole
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Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia
LGenome Res. 13 (6B), 1273-1289 (2003)
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                                                                                                                                                                                                                                      Similarity
92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (http://genome.gsc.riken.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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BY794229 RIKEN full-length enriched, 17.5 days embryo
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Contact: Yoshihide Hayashizaki
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1 (bases 1 to 331)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
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TGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 100
                                                                                                                                                                         ATGGTCCACTGCCCGCCGAGACACACAAACCCCAGCGAGCATTGAACACTGCACACGCCCATC
                                                       TGCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA
                                                                                                                    ATGGTCCACTGCCCGCGAGACACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTC 61
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                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="whole body"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="L930292H24"
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                                                                                                                                                                                                                                   Score 87.8; DB 6;
Pred. No. 1.3e-15;
0; Mismatches 7
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                 62
                                                                                                                                                                                                                                                                                                          N
              AI785818
401 bp mRNA linear EST 02-ui78h05.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1888569 5' similar to gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                        92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jag-Tel: 81-45-503-9222
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BY771317
insulin-like growth AI785818
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cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 354)
Carninci, P., Waki, K., Shiraki, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 13 (6B), 1273-1289 (2003)
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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BY771317
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                                                                                                                                                                                                                 TGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 100
                                                                                                                                                                                                                                                       TGCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 214
                                                                                                                                                                                                                                                                                                        ATGGTCCACTGCCGCGGAGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            visit our web site (http://genome.gsc.riken.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone 11.
'clone 11.
'le body"
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RIKEN full-length enriched, 17.5 days embryo whole body
ulus cDNA clone L930052G15 5', mRNA sequence.
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/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="C578L/6J"
/db_xref="taxon:10090"
/clone="L930052G15"
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Pred. No. 1
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RESULT 6
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AIII Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1887828 5' similar to gb:m59316 rnal INSULIN-LIKE GROWTH
FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:K81579 M.musculus
mRNA for insulin-like growth factor binding (MOUSE);, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FMAX: J14 200 2020
Email: mouseesFewatson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Other_ESTs: ui78h05.x1
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/WashU-NCI Mouse EST Project 1999
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 401)
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                                                                                                                                                                                                                                                                                                                                    TGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Sugano mouse liver mlia"
/note="Organ: liver, Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI shoul
be used to isolate the cDNA insert. Size selection was
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/lab_host="DH10B"
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92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 86.8; DB 1;
Pred. No. 2.8e-15;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 480)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lenmon,G., Soares,B., Wilson,R. and
A1530146
706 bp mRNA linear EST 18-MAR-1999 ui99f09,71 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1889609 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HŪMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                            91;
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AI196314.1
EST.
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1800
Fax: 314 286 1810
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Sugano mouse liver mlia"
/note="Torgan: liver; Vector: pME18S-FL3; Site 1: DraIII
(CACTGTGTG); Site 2: DraIII (CACCATGTG); lst Strand cDNA
was primed with an oligo(dT) primer
[ATGTGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:1887828"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 86.8; DB 1;
Pred. No. 2.9e-15;
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RESULT 8
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AI530146
AI530146.1
                    AI098594 inear EST 20-ue31e07.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1481988 5' similar to gb:X81579 m.musculus mRNA for insulin-like growth factor binding (MOUSE); mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       91;
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Email: mouseestewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                       GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 98
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                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME185-FL3; Site_1: DraIII
(CACCMTGTG); Site_2: DraIII (CACCMTGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATCTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME185-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/strain="C57BL"
/db xref="taxon:10090"
/clone="IMAGE:1889609"
/sex="female"
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lab_host="DH10B"
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92.9%;
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Pred. No. 3.1e-15;
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RESULT 9
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WashIn-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T. Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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EST.
Mus musculus (house mouse)
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This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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/note="Torgan: liver; Vector: pME18S-FL3; Site 1: DraIII
(CACCTGTGTG); Site 2: DraIII (CACCATGTG); lst Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor (TGTTGGCCTACTGG), digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Site selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/mol_type="mRNA"
/strain="C57BL"
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Pred. No. 3.
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                                                AI529939
ui87c09.yl Suga
IMAGE:1889392 !
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ui87c09.yl Sugano mouse liver mlia Mus musculus cDNA clone ui87c09.yl Sugano mouse liver mlia Mus musculus cDNA clone FACTOR EINDING PROTEIN I PRECURSOR (HŪMAN); gb.x81579 m.musculus mRNA for insulin-like growth factor binding (MOUSE); mRNA
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie; Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie; Marra, M., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schun Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCanu Materston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO Tel: 314 286 1800 Fax: 314 286 1810
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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AI530313.1
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                                                                                                                                                                                                                         GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 214
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//clone_lib="Sugano mouse liver mlia"
//note="Organ: liver; Vector: pME185-FL3; Site 1: DraIII (CACCATGTG); lst strand cDNA
(CACTGTGTG); Site 2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME185-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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/strain="C57BL"
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92.9%;
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Pred. No. 3.2e-15;
0; Mismatches 7;
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                                            811 bp
AGENCOURT 10789306 NIH MGC 152 Mus
IMAGE:6766752 5', mRNA sequence
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
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Location/Qualifiers
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314 286 1810
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//Clone_lib="Sugano mouse liver mlia"
//note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACCMTGTGTG); Site_2: DraIII (CACCMTGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ANGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). KhoI should
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sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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/clone="IMAGE:1889392"
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Pred. No. 3.2e-15;
0; Mismatches 7;
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                                                                                       musculus cDNA clone
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1st strand cDNA
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              Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Ghons,M., Pape,D., Harvey,N., Schurk,Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R. Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 848)
                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                uk28b10.y1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1970299 5' similar to gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Bradfield Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 811)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                 AI790802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLKW00138 row: m column: 23 High quality sequence stop: 536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTCCACTGCCCGCGGAGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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/db_xref="taxon:10090"
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92.9%;
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Pred. No. 3.2e-15;
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                                                                                                                                                                                                                                                                                                                                                                 mRNA
                                                            Cardenas, M., McCann, R.,
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                                                                            Schurk, R.,
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SOURCE
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AI528304
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              TITLE
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Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Pax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@mage.llnl.gov) for further information.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 852)

Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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852 bp mRNA linear EST 18-MAR-1999 ui95910;yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1890210 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HŪMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
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                                                                                                                                                                                                                                                                              musculus (house mouse)
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Location/Qualifiers
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//Clone lib="Sugano mouse kidney mkia"
//Clone lib="Sugano kidney; Vector: pWE18S-FL3; Site 1: DraIII
//CACCATGTGTG); Site 2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATCTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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/db_xref="taxon:10090"
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                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murina 1 (bases 1 to 605)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubgeisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B. Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Watterston
                                                                                                                                                                                                                                                                                                                                                            Bequence.
                                                                                                                                                                                                                                                                                                                                                                                                            All96154 linear EST 14-OCT-19 MRNA linear EST 14-OCT-19 MIG-9008.yl Sugano mouse lives mia Mus musculus cDNA clone IMAGE:1887663 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HŪMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
MGI:974534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forcest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                    Mus musculus
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EST.
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Location/Qualifiers
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           The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGTCCACTGCCCGCGGAGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Sugano mouse liver mlia"
//clone_lib="Sugano mouse liver mlia"
//note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTGG); Site_2: DraIII (CACCATGTG); lst strand cDNA
(CACTGTGTGGG); Site_2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATCTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTGTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mol_type="mRNA"
strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'dev_stage="adult"
'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="IMAGE:1890210"
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                                                                                                                                                                                                                                                                                                                                      GI:3748760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 86.8; DB 1; Length 852; Pred. No. 3.2e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                            Dietrich, N., Dubuque, T.,
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EST 14-OCT-1998

0

Gaps

XhoI should

3' end

Unpublished (1996)

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SOURCE
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VERSION
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TITLE
JOURNAL
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Best Local
                                                                                                                                                                             ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                          61
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 380)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                            Al785039 380 bp mRNA linear EST 02-
ui73a06.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1888018 5' similar to gb:X81579 M.musculus mRNA for
insulin-like growth factor binding (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _
                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                              AI785039
AI785039.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                    AI785039
                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGI:971987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: custom primer used
                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 214
                                                                                                                                                                                                                                                                                                                                                                                                        GCCCAGAGAGCTGTGACCACCACTGCCACTACTATCTA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                GI:5332755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No. 9.2e-15;
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Search completed:

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                            180 CAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 214
                                                                                                                                                120 TCCACTGCCCGCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCC 179
61
                                                                                                                                                                                                  87;
                                                                                                  1 TCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCATACGGCCGTCTGCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other ESTs: u173a06.x1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                      Similarity
  CAGAGAGCTGTGACCACCATTGCCACTACTATCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primer: custom primer used
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                /clone lib="Sugano mouse liver mlia"
/clone lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pMB18S-FL3; Site 1: DraIII
(CACCATGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence
                                                                                                                                                                                                                                                                                                                         sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dev_stage="adult"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'db_xref="taxon:10090"
'clone="IMAGE:1888018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mol_type="mRNA"
strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
                                                                                                                                                                                                                      37.5%;
                                                                                                                                                                                                  0
                                                                                                                                                                                                                      Score 82.2; DB 1;
Pred. No. 6.7e-14;
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                                                                                                                                                                                                  Mismatches
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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2 6/ptodata/2/pubpna/US07

2: /cgn2 6/ptodata/2/pubpna/US05

3: /cgn2_6/ptodata/2/pubpna/US05
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Copyright (c) 1993 - 2005 Compugen Ltd.
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gn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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2248.600 Million cell updates/sec
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219 219 219 219 219 219 76.4 76.4	Score
100.0 100.0 100.0 100.0 34.9 34.9	Query Match Length DB
219 270 321 372 423 1500	Length I
9 9 9 17	BB
US-09-972-916A-2 US-09-972-916A-3 US-09-972-916A-4 US-09-972-916A-5 US-09-972-916A-6 US-09-972-916A-6 US-09-917-800A-1608 US-10-388-934-5	ID
Sequence 2, Appli Sequence 3, Appli Sequence 4, Appli Sequence 5, Appli Sequence 6, Appli Sequence 1608, Ap Sequence 5, Appli	Description

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0-972-079-8 0-696-909A- 0-119-428-3 0-291-172-3 0-221-278-3	S-1-1-1	-10-425-115-28332 -10-282-122A-3325 -10-363-345A-4049 -10-363-345A-4049 -10-363-345A-4049	10-343-903-31 10-017-161-20 10-292-798-16 10-120-988-40 10-072-012-29 10-367-094-16	-10-027-632-164 -10-027-632-164 -10-011-585A-76 -10-741-601-574 -10-741-600-179 -10-437-963-791 -10-437-963-791	-191-803 -152-319 880-107- -893-315 -893-315 -311-455 -221-613
9259 51, 34, 31,	Sequence 40494, A Sequence 2769, Ap Sequence 1314, Ap Sequence 254, App Sequence 1, Appli	4 4 4 3 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4		164 164 76, 574 179 1791 7916 492	Sequence 73, Appl Sequence 1613, Ap Sequence 2393, Ap Sequence 1484, Ap Sequence 126, App Sequence 160, App Sequence 170, App Sequence 148, App

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US-09-972-916A-2
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APPLICANT: Thule, Peter M.
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                      SEQ ID NO 2
LENGTH: 219
                                                                                                                               Query Match 100.0%; Score 219; DB 9; Best Local Similarity 100.0%; Pred. No. 1e-68; Matches 219; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09972916A Patent No. US20020107198A1
                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Rattus norvegicus FEATURE:
Length 219;
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RESULT 3
US-09-972-916A-4
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US-09-972-916A-3
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                                                                        Sequence 4, Application US/09972916A
Patent No. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NO 4
LENGTH: 321
TYPE: NA
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LENGTH: 270
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Best Local
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TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION FILE REFERENCE: US 292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 6
             ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: Synthesized
                                                             TYPE: DNA
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Pred. No. 1.1e-68;
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Patent No. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 5
LENGTH: 372
Sequence 6, Application US/09972916A
Patent No. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
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Best Local Similarity
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US-09-917-800A-1608
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                                       PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOPTWARE: PATENTIN VET. 2.1
SEQ ID NO 1608
LENGTH:/1500
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Patent No. US20020119462A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR PILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 6
LENGTH: 423
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TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR APPLICATION NUMBER: US 60/222,880
                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
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ORGANISM: Rattus norvegicus
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                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/295,798 FILING DATE: 2001-06-06
                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/292,336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elashoff, Michael
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Pred. No. 1.2e-68;
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APPLICANT: MEDBRICK, Donna
APPLICANT: MODRACK, Donna
APPLICANT: JOHNSON, Kory
APPLICANT: HIGGS, Brandon
APPLICANT: CASTLE, Arthur
APPLICANT: ELASHOFF, Michael
TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
FILE REFERENCE: 44921-5090US
CURRENT APPLICATION NUMBER: US/10/191,803
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,819
PRIOR APPLICATION NUMBER: US 60/303,819
PRIOR PILING DATE: 2001-07-17
PRIOR FILING DATE: 2001-07-17
PRIOR FILING DATE: 2001-07-17
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US-10-191-803-73
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TYPE: DNA
; ORGANISM: Rattus norvegicus (No. US20040005547Alway rat)
US-10-388-934-5
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US-10-388-934-5
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Matches
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SEQ ID NO 5
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Publication No. US20040005547A1
GENERAL INFORMATION:
APPLICANT: Boess, Franziska
APPLICANT: Suter-Dick, Laura
APPLICANT: Wolf, Detlef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 02005336.9
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR FILING DATE: 2002-07-17
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nes 77; Conserv
APPLICATION NUMBER: US 60/369,351
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Pred. No. 6.2e-17;
0; Mismatches 1;
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Pred. No. 6.2e-17;
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; OTHER INFORMATION: Genbank Accession No. US-10-152-319A-1613
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APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR APPLICATION NUMBER: US 60/292,335
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US-10-152-319A-1613
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PRIOR FILLING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILLING DATE: 2001-06-13
PRIOR FILLING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILLING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR APPLICATION NUMBER: US 60/303,807
                                                                                                                                            SOFTWARE: Patentin
SEQ ID NO 1613
LENGTH: 1500
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  Query Match
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILING DATE: 2001-10-22
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                                                                                                                              TYPE: DNA
                                                                                    FEATURE:
                                                                                                        ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/324,928
FILING DATE: 2001-09-27
APPLICATION NUMBER: US 60/330,867
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/315,047 FILING DATE: 2001-08-28
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  Score 76.4;
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Pred. No. 6.2e-17;
0; Mismatches 1;
                                                            NM_013144
  DB 18;
Length 1500;
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US-10-756-149-1484
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US-09-880-107-2393
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LENGTH: 6128
TYPE: DNA
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
                                                                                                                                             Sequence 1484, Application US/10756149 Publication No. US20050181375A1
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Patent No. US2002014
GENERAL INFORMATION:
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Matches 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Genbank Accession No. US20020142981A1 M74587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                         593 GAGCATCGGCCACCGCCATCC
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                                                                                                                                                                                                                                                                                                                                                                                                     62 TAACCC----
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                                                                                                                                                                                                                                          CCACCCTCCCAGAGAGCACTGGCCACCGCTCC
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0020142981A1
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Pred. No. 4e-11;
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); Mismatches 1;
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                                                                                                                                                                                                                                                                                                         CATCCAGCGAGCATCTGCCGCCGCGCGCCG
                                                                                                                                                                                                                                             676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52;
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AND

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Sequence 126, Application US/10893315
PUBLICATION NO. US20050147987A1
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENTITLE OF INVENTION: WITH TYPE II DIABETES ANI
TITLE OF INVENTION: WITH TYPE II DIABETES ANI
TITLE OF INVENTION: WITH TYPE II DIABETES ANI
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000786
CURRENT APPLICATION NUMBER: US/10/893,315
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 2172
SOPTWARE: FABTSEQ for Windows Version 4.0
SEQ ID NO 126
                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 9173
; TYPE: DNA
; ORGANISM: Human
US-10-893-315-126
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US-10-893-315-126
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RESULT 13
US-10-893-315-160
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US-10-756-149-1484
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SEQ ID NO 1484
LENGTH: 6128
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Best Local Similarity
Matches 141; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                            62 TAACCC-----GIGCTGCCGAGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAGC
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                                                                                                      CCATCTGCCCAGAGAGCTGTGACCACCACTTC 202
                                                                                                                                            GAGCATCGGCCACCGCCATCC-----CATCCAGCGAGCATCTGCCGCCGCCGCCGCCG
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Pred. No. 4.4e-11;
0; Mismatches 52;
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Pred. No. 4e-11;
0; Mismatches 52;
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Sequence 970, Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
ITITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
FILE REFERENCE: 5013.1014
CCURRENT APPLICATION NUMBER: US/10/311,455
CCURRENT APPLICATION NUMBER: US/10/311,455
CCURRENT APPLICATION NUMBER: DCT/EP01/07537
PRIOR APPLICATION NUMBER: DC 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
                                                                                                     ; OTHER INFORMATION: chemically treated US-10-311-455-970
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Publication No. US20050147987A1
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN
TITLE OF INVENTION: WITH TYPE II DIABETES
TITLE OF INVENTION: USES THEREOP
FILE REFERENCE: CL000786
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SEQ ID NO 160
LENGTH: 9174
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
     Matches
                                                     Query Match
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CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                   LENGTH: 7061
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 2172
                                                                                                                                                        FEATURE:
  Local Similarity
les 48; Conserv
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  Conservative
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                        17.3%;
73.8%;
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Score 37.8; DB 15;
Pred. No. 0.0086;
0; Mismatches 17;
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Pred. No. 4.4e-11;
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                                                                                                                             DNA
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                                                Length 7061;
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  Gaps
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RESULT 15

US-10-221-613-148/c

iSequence 148, Application US/10221613

Publication No. US20040029123A1

GENERAL INFORMATION:
APPLICANT: DIEK, ALexander
APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle
FILE REFERENCE: 5013.1004

CURRENT APPLICATION NUMBER: US/10/221,613

CURRENT FILING DATE: 2002-09-13

PRIOR APPLICATION NUMBER: PCT/EP01/02945

DE 10013647.00
DE 10019173.8
DE 10043826.1
PRIOR FILING DATE: 2001-03-15

2000-04-06
2000-04-07
2000-06-30

- 2000-06-30
Search completed: September 1, 2005, 16:44:10 Job time: 647.824 secs
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                                                                                                                                                                                                                                                                                         ; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-221-613-148
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                                                                                                                                                                                                             Query Match 17.3
Best Local Similarity 73.8
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                               2000-09-01
NUMBER OF SEQ ID NOS: 428
SEQ ID NO 148
LENGTH: 7061
TYPE: DNA
                                                                                                                                           2185 CACTAACAAAACAAACTTATTTTAAACACTCAACTCCTAACGTACGACGCTACCAATCAT 2126
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                                                                                                       62 TAACC 66
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                                                                                                                                                                                                                 17.3%; Score 37.8; DB 17; 73.8%; Pred. No. 0.0086; ative 0; Mismatches 17;
                                                                                                                                                                                                                                                   Length 7061;
                                                                                                                                                                                                                   Indels
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Maximum
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Maximum Match 10
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Perfect score:
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length: 2000000000
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1: /cgn2_6/ptodata/1/ina/5A_COMB.Beq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.Beq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.Beq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.Beq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.Beq:*

6: /cgn2_6/ptodata/1/ina/backfIles1.Beq:*
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Match Length DB
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    Maximum Match 100%
Listing first 45 summaries
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    GenCore version (c) 1993 - 2005
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Compugen Ltd.
Sequence 30, Appl Sequence 19194, A Sequence 19184, A Sequence 73784, A Sequence 71, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 11745, A Sequence 11745, A Sequence 11790, A Sequence 11518, A Sequence 16518, A Sequence 16518, A Sequence 169692, A Sequence 13090, A Sequence 13090, A Sequence 13090, A Sequence 13093, A Sequence 13103, A Sequence 13103, A Sequence 13083, A Sequence 1241, Appl Sequence 17016, A Sequence 
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29 29 13.2 2194 4 US-09-270-767-10411 c 30 29 13.2 22054 4 US-09-270-767-10108 31 29 13.2 2454 4 US-09-252-991A-11217 31 29 13.2 2454 4 US-09-252-991A-11218 c 32 29 13.2 13489 4 US-09-949-016-15911 33 29 13.2 20235 1 US-07-642-734C-3 34 29 13.2 20235 1 US-07-642-734C-3 35 28.8 13.2 20235 3 US-08-439-009A-3 c 36 28.8 13.2 2439 3 US-09-67-782A-3 c 36 28.8 13.2 777 4 US-09-902-540-3367 37 28.8 13.2 1383 1 US-08-484-044-1 38 28.8 13.2 3182 1 US-08-484-044-1 39 28.8 13.2 3182 1 US-08-252-966B-11 40 28.8 13.2 3755 1 US-08-252-966B-17 41 28.8 13.2 3755 1 US-08-252-966B-17 41 28.8 13.2 3755 1 US-08-252-966B-17 41 28.8 13.2 11613 1 US-08-252-966B-17 41 28.8 13.2 11613 1 US-08-252-966B-17 42 28.8 13.2 11613 1 US-09-902-540-1158 43 28.6 13.1 1140 4 US-09-992-540-1158 44 28.6 13.1 1140 4 US-09-994-51-116
13.2 2194 13.2 2454 13.2 13489 13.2 20235 13.2 20235 13.2 20235 13.2 20235 13.2 20335 13.2 3183 13.2 3183 13.2 3183 13.2 3183 13.2 3183 13.2 3185 13.2 3759 13.2 3759 13.2 3759 13.2 3759 13.2 3759 13.2 3759 13.2 3759 13.2 3759 13.2 3765 13.1 1615 13.1 17125 4 13.1 1615
2 2194 2 2205 4 2 2454 4 2 2454 4 3 20235 1 2 20235 1 3 3 3 2 439 3 3 3 2 1383 1 2 3183 1 3759 1 17125 4 1 1615 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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4 US-09-270-767-10411 4 US-09-252-991A-11038 4 US-09-252-991A-11038 4 US-09-949-016-15911 1 US-07-642-734C-3 3 US-08-439-009A-3 3 US-08-439-009A-3 3 US-08-439-009A-1 1 US-08-448-044-1 1 US-08-484-044-1 1 US-08-252-966B-11 1 US-08-252-966B-17 1 US-08-252-956B-17 1 US-08-252-956B-17 1 US-08-252-956B-17 1 US-08-252-956B-17 1 US-08-252-956B-17 1 US-08-252-956B-17
US-09-270-767-10411 US-09-252-991A-11038 US-09-552-991A-11038 US-09-552-991A-11038 US-09-949-016-15911 US-07-6427-34C-3 US-08-439-009A-3 US-09-067-782A-3 US-09-067-782A-3 US-09-902-540-3367 US-08-484-044-11 US-08-252-966B-17 US-08-252-966B-17 US-08-252-961B-11

ALIGNMENTS

US-09-949-001-30

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; ORGANISM: Human
US-09-949-001-30
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Patent No. 6825336
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL000789
CURRENT PILING DATE: 2003-01-15
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/231,323
PRIOR APPLICATION NUMBER: 60/231,323
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ. ID NO 30
SEQ. ID NO 30
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.9
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 9173
  2049
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                                                                                                                     112 CAGCATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGC-ACACGG
                                                                                                                                                                                        62 TAACCC-----GTGCTGCCGAGCCAGCCCTTCATAAGGCCCTTGGGTATGGCCAGC
                                                                                                                                                                                                                                                                 2 CACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCAT
                       CCATCTGCCCAGAGAGCTGTGACCACCACTTC 202
CCACCCTCCCAGAGAGCACTGGCCACCGCTCC 2080
                                                                               GAGCATCGGCCACCGCCATCC-----CATCCAGCGAGCATCTGCCGCCGCGCGCCCC
                                                                                                                                                          TAACCTCCTGGTGCAAGTGGCGCGCGCTGTGCCCCTTTATAAGGTGCGCGCTGTGTCCAGC
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Pred. No. 8.8e-10;
0; Mismatches 52;
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US-09-949-001-36

Sequence 36, Application US/09949001
PATENT NO. 6825336
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL000789

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US-09-949-016-19194/c
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; ORGANISM: Human
US-09-949-001-36
                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19194
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19194, Application US/09949016
PATERIX INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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SEQ ID NO 36
LENGTH: 9174
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Best Local Similarity
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CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/231,323
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 848
                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                     Local Similarity
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                                                                           139 CAMACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCACCA 198
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  CTT 201
                                       CCCATCCAGAGACACCCCCGCATCACAGCCCTGCCACCACCACTCCATGCATAGCC
                                                                                                                     CCAGGCCTTCCTGGGGCGCTGTTCCTCCATCCAGCTTAGCCACCTGCCAGGTTAGGCC
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                                                                                                                                                                                                                     16.0%;
55.3%;
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Pred. No. 8.8e-10;
0; Mismatches 52;
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Matches

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Indels

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US-09-949-016-2153
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US-09-949-016-73784/c
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILLING DATE: 2000-10-03
PRIOR FILLING DATE: 2000-09-08
PRIOR FI
                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2153
LENGTH: 2393
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6812339
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/99/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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ORGANISM: Human
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les 68; Conserv
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16.0%;
ilarity 55.3%;
Conservative
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55.3%;
Score 35; DB 4
Pred. No. 0.18;
0; Mismatches
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Pred. No. 0.11;
0; Mismatches
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                                                                                  DB 4; Length 2393;
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US-09-949-016-74/c
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US-09-949-016-74
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Best Local S
Matches 68
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 74
LENGTH: 2408
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                         Sequence 11816, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PRIOR DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                   APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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RESULT 9 US-08-304-309-3

Sequence 3, Application US/08304309 Patent No. 5856454 GENERAL INFORMATION:

APPLICANT:

GONZALEZ,

Frank J.

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; LENGTH: 7562
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241.755
PRIOR APPLICATION NUMBER: 60/241.756
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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; ORGANISM: Human
US-09-949-016-11816
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SOFTWARE: FRATSEQ for Windows
SEQ ID NO 11816
LENGTH: 7561
                                                                                                                                                                                                                                   Query Match
Best Local
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LENGTH: 7562
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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les 68; Conserv
5230
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                                                                       CCCATCCAGAGACACCACCCGGATCACAGCCCTGCCACCACCACCATGCATAGCC 5231
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Pred. No. 0.28;
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OF DETECTION AND USES THEREOF
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US-08-991-942-3
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NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPHAX: (415) 543-9600
TELEPHAX: (415) 543-9603
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4447 base pairs
                                                                                                                                            Sequence 3, Application US/08991942
Patent No. 6015673
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                  NUMBER OF SEQUENCES: 1
                                                                      APPLICANT: GONZALEZ, Frank J.
APPLICANT: FERNANDEZ-SALGUERO, Pedro
TITLE OF INVENTION: CLONING AND EXPRESSION OF CDNA
TITLE OF INVENTION: DIHYDROPYRIMIDINE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRATURE:
NAME/KEY: misc_feature
LOCATION: 1..4447
OTHER INFORMATION: /product= "Pig_DPD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,309
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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MEDIUM TYPE: Floppy disk
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 ADDRESSEE:
STREET: SI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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                                                                                                                                                                                                                                                                                                 ACACGGCCATCTGCCCAGAGAGCTGTGACCACCACCTTCCGCTACT 209
                                                                                                                                                                                                                                                                                                                                               CCCTGGCCAGCGGTGGGTGCTGGCAAGCGGACTACATACGGAGGAGTGTCTGGCACGGCC
                                                                                                                                                                                                                                                                                                                                                                                    GGCCAGCCAGCATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGC
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Steuart Street Tower,
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seuart Street Tower, One Market Plaza
Townsend and Townsend Khourie and Crew euart Street Tower, One Market Plaza
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                                                                                        CLONING AND EXPRESSION OF CDNA FOR HUMAN
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Pred. No. 1.9;
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RESULT 11
US-09-949-016-11745
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                                 PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
                                                                                           CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                              APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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INFORMATION FOR SEQ ID NO:
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FILING DATE: 09-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
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LOCATION:
FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                      CCCTGGCCAGCGGTGGGTGCTGGCAAGCGGACTACATACGGAGGAGTGTCTGGCACGGCC 2394
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California
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88..3162
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                                                                                       2000-04-14
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49.7%;
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Pred. No. 1
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OF DETECTI
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Sequence 16163, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
RESULT 13
US-09-774-528-404/c
US-09-774-528-404/c
; Sequence 404, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
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; ORGANISM: Human
US-09-949-016-16163
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US-09-949-016-16163
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; ORGANISM: Human
US-09-949-016-11745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16163
LENGTH: 36181
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 11745
LENGTH: 36180
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Best Local Similarity
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 11990
LENGTH: 99748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo 9
; CAGANISM: Homo 9
; PEATURE:
; NAME/KEY: CDS
; LOCATION: (194).
US-09-774-528-404
                                                                     ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11990
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US-09-949-016-11990/c
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 Query Match
Best Local S
Matches 64
                                                                                                                                                                                                                                                                                                                                 Sequence 11990, Application US/09949016
PATENT NO. 6812339
GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
FILE REFERENCE: CL001307
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Best Local Similarity 58.5%;
Matches 55; Conservative
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CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
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SOFTWARE: pt_FL_genes Version 2.0
                                                                                                          LENGTH:
TYPE: DI
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TITLE OF INVENTION: No. 6743619el Nucleic
TITLE OF INVENTION: Polypeptides
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 64; Conserv
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Zhao, Qing A.
Yang, Yonghong
Xue, Aidong J.
Wehrman, Tom
Wang, Jian-Rui
Wang, Dunrui
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di, Vinod
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                  14.4%;
Score 31.6; Di
Pred. No. 10;
0; Mismatches
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Pred. No. 1.9;
0; Mismatches 39;
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                                  DB 4;
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RESULT 15
US-09-949-016-16518/C
Sequence 16518, Application US/09949016
Patent No. 6812239
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-0
Search completed: September 1, Job time: 73.3315 secs
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                                            2005, 07:07:07
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Perfect score:
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Match Length
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Maximum Match 100%
Listing first 45 summaries
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G19994 BWSS752 Eri
M59316 Human insul
M59316 Human insul
AY434089 Homo sapi
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BC013345 Mus muscu
AY560836 Spermophi
AX401932 Sequence
AX827271 Sequence
MS8634 Rat IGF bin
AX163782 Sequence
L22979 Rat insulin
BC078889 Rattus no
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BV184757 sqnm14591	AE016922 Chromobac	AL713999 Human DNA	AY316591 Homo sapi	U47654 Homo sapien	Z18922 H.sapiens D	BX640447 Bordetell	BX640427 Bordetell	BX640428 Bordetell	AX348680 Seguence	AX345899 Sequence	AX251887 Sequence	AC097039 Rattus no	M17088 Rat pyruvat	M89791 Rattus norv	G67173 IGFBP1 5'A	M23592 Human insul	X05684 Rat L-PK ge	AX827302 Sequence	E14395 gDNA encodi	AR175909 Sequence	A57715 Sequence 1	AC148834 Pan trogl	AC146117 Pan trogl	AC146152 Pan trogl	AC091524 Homo sapi

ALIGNMENTS

REFERENCE AUTHORS JOURNAL KEYWORDS SOURCE ORGANISM LOCUS DEFINITION ACCESSION RESULT 1 RATILGFZ ORIGIN FEATURES COMMENT VERSION source 1 (bases 1 to 1181) Unterman,T.G., Lacson,R.G., McGary,E., Whalen,C. and Goswami,R. Biochem. Biophys. Res. Commun. (1991) In press Original source text: Rattus norvegicus (strain Sprague-Dawley) male adult liver DNA. RATILGFZ 1181 bg Rattus norvegicus insulin-like M84484 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; insulin-like growth factor. Rattus norvegicus (Norway rat) Rattus norvegicus M84484.1 GI:204927 Rattue. /sex="male" /tissue_type="liver" /dev_stage="adult" /organism="Rattus norvegicus" /mol_type="genomic DNA" /strain="Sprague-Dawley" /db_xref="taxon:10116" Location/Qualifiers 78.7**%**; 99.5**%**; Score 212.4; DB Pred. No. 3e-52; 0; Mismatches đđ Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; growth DNA facter linear er gene and Goswami, R.G. fragment. ROD 27-APR-1993

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883

172 CCACTGCCCGCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC

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52 TCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA 111

TCACAAGCAAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA

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Matches 213;

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Query Match Best Local Similarity

DB 10; Length 1181;

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AC136382
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                                                            TITLE
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                                                                                                                                                                                                                                                                                          Allen, C., Allen, Metker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Barden, H., Baden, H., Badwin, D., Bandaranaike, D., Barber, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bliswalo, K., Blair, J., Blarkenburg, K., Blyth, P., Brown, M., Benahmed, F., Bryant, N., Bahay, C., Burch, P., Burrell, K., Caldesron, E., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cheveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D., Souza, L., Davis, C., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Chen, Y., Chen, Y., Chen, Z., Chu, J., Chen, Y., Chen, Y., Chen, Z., Chu, J., Chen, Y., Chen, Y., Chen, Y., Chen, Z., Chu, J., Chen, Y., Chen, Y., Chen, Z., Chu, J., Chen, Y., Chen, Z., Chen, Z., Chu, J., Chen, Z., Chu, J., Chen, Z., Chu, J., Chen, Z., Chu, J., Chen, Z., Chen, 
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                                                                         Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X., Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Waite, P., Williams, G., Wilson, R., Waeczyk, R., Warren, R., Waite, P., Williams, G., Wilson, R., Waeczyk, R., Woden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
            Unpublished
2 (bases 1 to 185148)
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AC136382.1 GI:24462257
HTG; HTGS PHASE1.
Rattus norvegicus (Norway rat)
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                                                              Direct Submission
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 265
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Genome Sequencing Consortium
                                                                                                                                                                                                                                               Sutton, A.,
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Baylor Plaza, Houston, TX 77030, USA
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 135613 bases at least Q40
Consensus quality: 140849 bases at least Q30
Consensus quality: 145680 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/
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46631: contig of 1983 b
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50702: gap of unknown 1
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59049: gap of unknown 1
62942: contig of 1810 b
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67235: contig of 3003 b
68197: gap of unknown 1
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2 (bases 1 to 1363)
Mohn,K.L., Waddle,J.R. and Taub,R.
Comparison of mouse and human IGFBP-1
Comparison of sequence and conser
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insulin-like growth factor binding protein-1.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-JUL-1992) R.A. Taub, Univ. of Pennsylvania, Howard Hughes Medical Institute, Clinical Research Bldg., Room 475, 422 Curie Boulevard, Philadelphia, PA 19104-6145, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mohn,K.L., Bucan,M. and Taub,R. Structure and localization of the IGFBP-1 gene and its expression during liver regeneration Hepatology 19 (3), 656-665 (1994) 94164648
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3 (bases 1 to 1363)
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                                                                                                                                                               sequences"
764. .768
792. .1336
                                                                                                                                                                                                                                                                                              500.
                                                                                                                                                                                                                                                                                                     /cell_line="NIH 3T3"
/cell_type="fibroblast"
/clone_lib="genomic, lamb
/dev_stage="embryo"
500__stage="embryo"
/codon_start=1
/product="insulin-like growth factor
/protein_id="CAN47832.1"
/db_xref="GOA:P47876"
/db_xref="GOA:P47876"
                                                                                                 /note="mRNA
964. .>1336
                                                                                                                                                 number=1
                                                                                                                                                                                                              note="Caat
                                                                                                                                                                                                                                                                            note="AP-2
                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="NIH Swiss"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                            note="insulin-responsive element"
                                                                                                                                                                                                                                                                                                                                                                           clone="JW2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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                                                                                                                 site"
                                                                                                                                                                                                               with APF, HNF and NF-El consensus
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                                                                   factor binding protein-1"
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intron/exon
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RESULT 4
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                               source
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                                                                                                                                                                                                                                                      AL Submitted (11-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 12, 2002 this sequence version replaced gi:19847866.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Mp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    857
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                                                                                                                                                constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-20C9 from the RPCI-23 Mouse PAC Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse DNA sequence from clone
                                                                                                                                                                                                                                               database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oliver, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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HTG.
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                                                                                                                          pBACe3.6.
/organism="Mus musculus
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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PVPASCPEISRPAGCGCCPTCALPMGAACGVATARCAQGLSCRALPGEPRPLHALTRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGASLPEPAAPATSTLFSSQHE"
                                                                                                 location/Qualifiers
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92.5%;
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Pred. No. 4.3e-45;
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m clone RP23-20C9 on chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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TITLE
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BC013345
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                                                                                                                                                                                                                                                                                                                                                                                                Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsteh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bossak, S.A., McEwan, P.J.,

McKernan, K.J., Malak, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Pahey, J., Helton, E., Ketteman, M., Madan, A., Kodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Bouffard, G.G., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                             NIH-MGC Project URL: http://mgc.
Contact: MGC help desk
                                                                                                                                                                                       Direct Submission
Submitted (31-AUG-2001) National Institutes of Health, Mammalian Submitted (71-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BC013345 1569 bp mRNA linear ROD 30-JUN-Mus musculus insulin-like growth factor binding protein 1, mRNA (CDNA clone MGC:14075 IMAGE:4161889), complete cds.
                                                                                                                                                                                                                                                                                                                          Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAGAGCTGTGACCACCATTGCCACTACTATCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCACAAGCAAAACATATTTTGAACACTGGGGTCCTAGCACGCTGCCCTGACAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 1569)
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/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.8%;
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Pred. No. 4.3e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2004
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SOURCE
ORGANISM
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DEFINITION
                                                                                                                                                                                                                                                                    RESULT 6
AY560836
                                                        REFERENCE
                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                   VERSION
                                                                                                                                                                                                  ACCESSION
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Best Local S
Matches 103
                      AUTHORS
TITLE
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Li,Y., Klimanis,D. and Hallenbeck,J.M. Cloning and characterization of insulin-like growth factor binding protein 1 (IGFBP-1) from thirteen-lined ground squirrel
                                                                                                                                                                                                                  Spermophilus tridecemlineatus protein 1 (IGFBP1) mRNA, compl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 18 Row: i Column: 20
This clone was selected for full line: equencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton,
                                                                         Spermophilus
                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                            Spermophilus tridecemlineatus (thirteen-lined ground squirrel)
Spermophilus tridecemlineatus
                                                                                                                                                                                 AY560836.1 GI:45505308
                                                                                                                                                                                                                                                     AY560836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Madan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                              CACACGGCCATCTGCCCAGAGAGAGCTGTGACCACCACCACCTTCCGCTACTAGCTA 265
                                                                                                                                                                                                                                                                                                                                          CACACGGCCGTCTGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACACACAACCCCAGCGAGCATTGAACACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                 1 (IGFBP1) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="insulin-like growth factor binding protein 1"
/protein_id="AAH13345.1"
/db_xref="GI:15426483"
/db_xref="HOCUSID:16006"
/db_xref="MGI:96436"
/translation="MPEFLTVVSWPFLILLSFQIGVAAGAPQPWHCAPCTAERLGLCP
PVPASCPEISRPAGGGCTPCALPMGAAGGVATARCAQGLSCRALPGEPRPLHALTRG
GGACVPEPAAPATSTLSSSQHEEAKAAVVSADELSESPEMTEEGLLDSFHLMAPSRED
GDILWAAISTYSSMRAREIADLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
PRIMARISTYSSMRAREIADLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNKNGFYHSKQCETSLDGEAGLCWCVYPWSGKKIPGSLETRGDPNCHQYFNVHN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="synonym: IGFBP-1"
/db_xref="LocusID:16006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="MGI:96436"
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/strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="MGC:14075 IMAGE:4161889"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 98.2; DB 10;
Pred. No. 3.2e-18;
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                                                                                                                                                                                                                 complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                      Craniata; Vertebrata; Eut
Sciurognathi; Sciuridae;
                                                                                                                                                                                                                                 insulin-like
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growth
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                                                                                                          Euteleostomi;
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                                                                                           Sciurinae;
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ACCESSION
VERSION
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ORGANISM
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AX401932
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                                                                                                                                                             JOURNAL
                                                                                                                                                                                TITLE
                                                                                                                                                                                                                  AUTHORS
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ORIGIN

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Query Match
Best Local Similarity
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                            1500 bp | 1
Sequence 1608 from Patent W00210453
AX401932
                                                                                                                                                                            Mendrick, D.,
Elashoff, M.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li,Y., Klimanis,D. and Hallenbeck,J.M.
Direct Submission
Submitted (27-FBB-2004) StrokeBranch, NINDS/NIH,
Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Norway rat)
                                                                                                                      Gene Logic,
                                                                                                                                           Patent:
                                                                                                                                                              Molecular toxicology
                                                                                                                                                                                                                                                                                                                                                             AX401932.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCATCTGCCCAGAGAGCTGTGACCACCACTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAAGCATCGTGCACTGCCCACGGCGACTCAGAATTGGACACCTATCAA-----GCCACT
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Y., Klimanis,D. a
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                                                                                                                                         WO 0210453-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MPEVPAAGLWPFILLLAVQVSTVASSTQPWHCAPCSAEKLALCP PVPSSCPELSRPAGCGCCPMCALPLGARGCWATARYARGLSCRALPGEPRPLHALTRG OGACVPEPATPTASGLSS IEKEEAKAGMVPERVPPESAEMTERGLLES FHLMASSSED QPILWMAISTYKSMRAREMADIKKWKQPCRRELYKVLERLAKAQQKAGBEIYKFVLPN CNKNGFYHSKQCETSLDGEAELCWCVYPWSGRRIPGSLEIRGDPNCHQYFNVQN"
                  organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="insulin-like
/protein_id="AAS67029.]
/db_xref="GI:45505309"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="IGFBP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Spermophilus tridecemlineatus"
/mol_type="mRNA"
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note="EMBL/GenBank Accession No. NM_013144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="IGFBP1"
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                                                                                                                                                                                                                                                                                                                                                             GI:21338112
                                                                                                                        Inc.
                                                                                                                                                                                                 Porter, M.W., Johnson, K.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCGTGCTGCCGAGCCAGCCCTTCATAAGGCCCTGGGTATGGCCA 160
                                                                                                                                                                                                                                                            Chordata;
Rodentia;
                                                                                                                                         1608 07-FEB-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 76.6; DB 10
Pred. No. 8.8e-12;
0; Mismatches 54
                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e growth factor
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                                                                                                                                                                                                   Castle, A.L. and
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Best Local S
Matches 77
                                                                JOURNAL
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                                                                                                      AUTHORS
TITLE
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TITLE
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                                                             Reduces.

1 (bases 1 to 1500)

1 (bases 1 to 1500)

1 (bases 1 to 1500)

The gene encoding rat insulinlike growth factor-binding is rapidly and highly induced in regenerating liver Mol. Cell. Biol. 11 (3), 1393-1401 (1991)
                                                                                                                                                                                                                                                                                                                                       83
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                                                                                                                                                                                  M58634.1 GI:204732
IGF binding protein-1.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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                                      Original
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                    RATIGFB 1500 bp mRNA Rat IGF binding protein-1 (rIGFBP-1) mRNA,
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Rattus norvegicus
Eukaryota, Metazoa, Chordata,
Mammalia; Eutheria; Rodentia;
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Sequence 5 from Patent I
AX827271
AX827271.1 GI:39837360
                                                                                                                                               Rattus.
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                                                                                                                                                                                                                                                                                                                                                    CACTTCCGCTACTAGCTA 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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            source text: Rat, cDNA to mRNA. Location/Qualifiers
1. .1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
organism="Rattus norvegicus"
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Sciurognathi; Muridae;
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Matches 77
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AX163782
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Patent: WO 0138579-A 46 31-MAY-2001;
Curagen Corporation (US)
Location/Qualifiers
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77; Conserv
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Mammalia; Eutheria;
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CACTTCCGCTACTATCTA 78
                                              CACTTCCGCTACTAGCTA 265
                                                                                                     CACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
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46 from Patent WO0138579.
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                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
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/tissue_type="regenerating
/dev_stage="adult"
160._.978
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/product="IGF binding
/protein_id="AAA41380.
/db_xref="GI:204733"
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/strain="Fisher"
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                                                                                                                                                                                                        Score 76.4; DB 6;
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Pred. No. le-11;
0; Mismatches 1;
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RESULT 11 RATIGFBA

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                     188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L22979.1 GI:1098472
insulin-like growth factor binding
Rattus norvegicus (Norway rat)
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L22979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Nov 30, 1995 this sequence version replaced gi:385167.
Original source text: Rattus norvegicus (strain Sprague-Dawley)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                               Similarity
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CACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
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QGACVLEPAAPATSSLSGSQHEEAKAAVASEDELAESPEMTEEQLLDSFHLMAPSRED
QPILMNAISTYSSMRAREITDLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="IGFBP-1"
join(153. .525,1850.
/gene="IGFBP-1"
                                                                                                                                                                                                   3003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="insulin-like growth factor binding protein"
/protein_id="AAA82581.1"
/db xref="Gi:1098473"
/translation="MPEFLTVVSWPFLILLSFQVRVVAGAPQPWHCAPCTAERLELCP
                                                                                                                                                                                 3003. .4089
/gene="IGFBP-1"
                                                                                                                                                                                                                                                                       /gene="IGFBP-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /number=1
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                                                                                                                                                                                                                              gene="IGFBP-1"
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                                                                                                                                                                                                                                                                                                                                                                  'gene="IGFBP-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="liver"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'sex="male"
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                                                              28.3%;
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                                              Score 76.4; DB 10;
Pred. No. 1e-11;
0; Mismatches 1;
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; Murinae;
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ORGANISM
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KEYWORDS
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TITLE
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RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKornan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marrs, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences
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                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 114 Row: e Column: 20 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6981079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Howard_Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Director MGC Project.

Direct Submission

Direct Submission

Submitted (02-AUG-2004) National Institutes of Health, Mammalian Submitted (02-AUG-2004). Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.
Dickson, M., Schmutz, J., Grimwood, J., Rodri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Institute, 31 Center Drive, Room
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                      Kim,J.J., Taylor,H.S., Akbas,G.E., Foucher,I., Trembleau,A., Jaffe,R.C., Fazleabas,A.T. and Unterman,T.G. Regulation of insulin-like growth factor binding protein-1 promoter activity by FKHR and HOXA10 in primate endometrial cells Biol. Reprod. 68 (1), 24-30 (2003)
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                                                                                                                                                                                                               Direct Submission
Submitted (11-APR-2002) Department of Obstetrics and Gynecology,
Submitted (11-Ilinois at Chicago, 820 S. Wood, Chicago, IL 60612,
                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 3886)
Kim, J.J., Jaffe, R.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Papio anubis (olive baboon)
Papio anubis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AY095345.1 GI:20853764
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142...960
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PVPASCFORD
PVPASCFORD
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                                                         /organism="Papio anubis"
/mol_type="genomic DNA"
/db_xref="taxon:9555"
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/gene="IGFBP-1"
                                                                                                                                                                                      Location/Qualifiers
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/lab_host="DH10B"
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Tel: +33-4-72738698
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Mammalia; Eutheria; Primates; Catar
1 (Dases 1 to 448)
Cox,D.G., Boillot,C. and Canzian,F.
                                                                                                                                                                                                                                                                                                                                          Contact: Federico Canzian
                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                    Primer B:
                                                                                                                                                                                                                                                                Fax: +33-4-72738388
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Primer:
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A: TGCACTAGCAAACAACTT
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3655. .3886
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AUTHORS
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Bource
                                                                                                                                                                                                                  Query Match 22.5
Best Local Similarity 66.5
Matches 141; Conservative
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 2394 from Patent WO0229103.
AX409747 GI:21442452
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CCATCTGCCCAGAGAGCTGTGACCACCACTTC 253
                              GAGCATCGGCCACCGCCATCC-----CATCCAGCGAGCATCTGCCGCCGCGCGCCGCCG
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1. .448
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66.5%; Pred. No. 4.5e-07;
ative 0; Mismatches 52
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A1529939 ui87c09.y
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SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 1 BF236974 ORIGIN FEATURES COMMENT REFERENCE DEFINITION POCUS TITLE JOURNAL Query Match Best Local Similarity Matches 103; Conserv AUTHORS source Email: cgapbs-r@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM9443 row: j column: 02 High quality sequence stop: 581. Location/Qualifiers NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1013) Mus musculus (house mouse) BF236974 1013 602026605F1 NCI_CGAP_Li9 Mus Contact: Robert Strausberg, Ph.D. BF236974.1 GI:11150891 BF23697 mRNA sequence. /db_xref="taxon:10090" /clone="IMAGE:416.1889" /lab_host="PH108 (T1 phage-resistant)" /clone_lib="NCI CGAP_Li9" /clone_lib="NCI CGAP_Li9" /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library." organism="Mus musculus" /mol_type="mRNA" /strain="FVB/N" . .1013 36.4%; Score 98.2; DB 2; Pred. No. 1.5e-18; 0; Mismatches 8; bp mRNA linear EST 14-NOV-2000 musculus cDNA clone IMAGE:4161889 5', Length 1013; Muø.

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                                                                       N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
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Mus musculus cDNA clone L930176D05 5', mRNA sequence.
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Carninci, P., Waki, K., Shiraki, T.,
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/dev stage="17.5 days embryo"
/clone libb"RIKEN full-length enriched, 17.5
whole body"
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/mol_type="mRNA"
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/clone="L930176D05"
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The Institute of Physical and Chemical Research (RIKEN)
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Division of Experimental Animal Research in Riken contributed to
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Mammalia; Eutheria;
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TGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 100
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                                                                                        ATGGTCCACTGCCCGCGGAGACACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTC
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visit our web site (http://genome.gsc.riken.jp/)
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RIKEN full-length enriched, 17.5 days embryo
ulus cDNA clone L930292H24 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                whole body"
                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                           /tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                     clone="L930292H24"
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Rodentia;
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                                                                                                                                                                                              Score 87.8; DB 6;
Pred. No. 1.6e-15;
                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN Genomic
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RESULT 5
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Best Local Similarity
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1 (bases 1 to 354)

1 (bases 1 to 354)

2 Carninci, P., Waki, K., Shiraki, T., Konno, H., Shibata, K., Itoh, M., Aizawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S., Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watahiki, A., Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A., Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K., Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K., Pavan, W., Aidinis, V., Nakagawara, A., Held, W.A., Iwata, H., Kono, T., Nakauchi, H., Lyons, P., Wells, C., Hume, D.A., Fagiolini, M., Nakauchi, H., Lyons, P., Wells, C., Hume, D.A., Fagiolini, M., Hensch, T.K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P., Muramatsu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y. Targetling a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia
Genome Res. 13 (6B), 1273-1289 (2003)
                                                                                                                                                                                                                                                                                  227
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                                                                                                                                                                                                                                62
                                          AI785818 401 bp mRNA linear EST 02. ui78h05.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE: 1888569 5' similar to gb:X81579 M.musculus mRNA for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genom
Sciences Center(SC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehito-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045,
Tel: 81-45-503-9216
Fax: 81-45-503-9216
insulin-like
AI785818
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Please visit our web
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BY771317.1 GI:39697955
EST.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                     TGCCCAGAGCTGTGACCACCACTTCCGCTACTAGCTA
                                                                                                                                                                                                                                TGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA
                                                                                                                                                                                                                                                                                                                                ATGGTCCACTGCCCGCGAGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTC
                                                                                                                                                                                                                                                                                                                                                                ATGGTCCACTGCCCGCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          visit our web site (http://genome.gsc.riken.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 bp mRNA linear EST 23-N
RIKEN full-length enriched, 17.5 days embryo whole
ulus cDNA clone L930052G15 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
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/clone="L930052G15"
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                     growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.5%;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                     binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.8; DB 6;
No. 1.7e-15;
                  (MOUSE);, mRNA sequence
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                                                                                                  EST 02-JUL-1999
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DEFINITION

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RESULT 6
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                                                                                                                                                                                                                                                                   228 GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 265
                                                                                                                                                                                                                                                                                                                                                                                168 TGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCT
AI196314

Wis musculus cDNA clone ui71207.yl Sugano mouse liver mlia Mus musculus cDNA clone IMACE:1887828 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus factor binding (MOUSE);, mRNA
                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                              91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Other_ESTs: ui78h05.x1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 401)
                                                                                                                                                                                                                                  GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA
                                                                                                                                                                                                                                                                                                                             TGGTCCACTGCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: .
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
(CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI shoul
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing; 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="adult"
/lab_host="DH10B"
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strain="C57BL"
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92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 86.8; DB 1;
Pred. No. 3.4e-15;
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AUTHORS
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                                                                                 DEFINITION
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AIS30146
706 bp mRNA linear with the uis9f09.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1889609 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus factor binding (MOUSE);, mRNA
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AI196314.1
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 480)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T. Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterstor
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The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                     GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 265
                                                                                                                                                                                                                                                                                                      TGGTCCACTGCCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer: custom primer used h quality sequence stop: 375.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME185-FL3; Site_1: DrallI
(CACTGTGTGT); Site_2: DrallI (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DrallI adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DrallI sites of the pME185-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). Xhol shou
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
Constructed by Dr. Surio Scoren (Intercett).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' primer CGACCTGCAGCTCGAGCACA."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="C57BL"
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92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 86.8; DB 1;
Pred. No. 3.6e-15;
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RESULT 8
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AI530146
AI530146.1
               AIO98594 TRNA linear EST 20-ue31e07.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1481988 5' similar to gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                              μ.
                                                                                                                                                                                                                                                                                                                                                                                                        91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R. Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                  GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 98
                                                                                                                                                                                                                                                                                                            TGGTCCACTGCCCGCGAGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=Torgan: liver; Vector: pMEI8S-FL3; Site 1: DraIII (CACTGTGTG); Site 2: DraIII (CACCATGTG); lst strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pMEI8S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCACA."
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| db_host="DH10B"
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mol_type="mRNA"

strain="C57BL"
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Pred. No. 3.9e-15;
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1800
Fax: 314 286 1810
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The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Sugano mouse liver mlia"
//clone_lib="Sugano mouse liver mlia"
//note="Organ: liver; Vector: pMEL8S-FL3; Site_1: DraIII
(CACCATGTGTG); Site_2: DraIII (CACCATGTG); 1st Strand cDNA
was primed with an oligo(dT) primer
[ANGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG]. Diagested
and cloned into distinct DraIII sites of the pMEL8S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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/clone="IMAGE:1481988"
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92.9%;
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RESULT 10
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KEYWORDS
SOURCE
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                                                                                    DEFINITION
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Best Local Similarity
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                                                                                                                                                                                                                                                                    228 GCCCAGAGAGCTGTGACCACCACCTTCCGCTACTAGCTA 265
                                                                                                                                                                                                                                                                                                                                                                                                 168
                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                  91;
A1529939 799 bp mRNA linear EST 18-MAR-15 ui87c09,yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1889392 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HŪMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
                                                                                                                                                                                                                                                                                                                                             1 TGGTCCACTGCCCGCGGAGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R. Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
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EST.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pMELBS-FL3; Site 1: DraIII
(CACTGTGTG); Site 2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ANGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pMELBS-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 86.8; DB 1;
Pred. No. 4e-15;
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                                                                                                         EST 18-MAR-1999
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sequence

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ACCESSION
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                                                   811 bp
AGENCOURT 10789306 NIH MGC 152 Mus
IMAGE:6766752 5', mRNA sequence
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1 (bases 1 to 799)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptce, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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AI529939.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                         GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 265
                                                                                                                                                                                                                                                                                                                                                  TGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCT
                                                                                                                                                                                                                               GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 98
                                                                                                                                                                                                                                                                                                                        TGGTCCACTGCCCGCGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(AACTGTGTG); Site_2: DraIII (CACCATGTG); 1st Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTGTCTGCTTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/strain="C57BL"
/db_xref="taxon:10090"
/db_me="TAKGE:1889392"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:4444074
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                                                                                                                                                                                                                                                                                                                                                                                                                                    32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 86.8; DB Pred. No. 4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                           musculus
                                                                                                                mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Length 799;
                                                                                                              linear
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                                                                                           cDNA clone
                                                                                                                EST 09-MAR-2004
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AI790802
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                DEFINITION
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                                                                                                                                                                                           ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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 JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 TGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91;
                 Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,IRitter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R. Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                      A1790802 848 bp mRNA linear EST 02-c uk28b10.y1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1970299 5' similar to gb:x81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Mark Bittinger
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLKM00138 row: m column: 23
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Unpublished (1999)
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                  AI790802.1
EST.
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Tissue Procurement: Bradfield Laboratory
                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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Unpublished (1999)
                                                                                                                                   1 (bases 1 to 848)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6766752"
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                                                                                                                                                                                                                                                    GI:5338518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.1%;
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Pred. No. 4e
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                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                           Cardenas, M., McCann, R.,
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                                                                           Schurk, R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                                                                                                                                                                                                                               SOURCE
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Matches
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                                           1 (bases 1 to 852)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R. The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                          Mus musculus
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Other_EST8: uk28b10.xl
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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Location/Qualifiers
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/clone libs"Sugano mouse kidney mkia"
/clone libs"Sugano mouse kidney mkia"
/note="Organ: kidney; Vector: pME18S-FL3; Site 1: DraIII
/note="Organ: kidney; Vector: pME18S-FL3; Site 1: DraIII
/CACTGTGTG); Site 2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATGTGCCTTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 86.8; DB 1; Length 848; Pred. No. 4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                        Murinae; Mus
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                                                                                             Schurk, R.,
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VERSION
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AI196154
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   TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 TGGTCCACTGCCCGGCGAGACACAAAACCCAGCGAGCATTGAACACTGCACACGGCCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91;
                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murina-1 (bases 1 to 605)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubi Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B. Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
AI196154
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                                 Waterston, R
                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:974534
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                    AI196154.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: custom primer used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Clone_lib="Sugano mouse liver mlia"
//clone_Torgan: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACCTGTGTG); Site_2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). Xhol should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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|lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
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92.9%;
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Pred. No. 4e-15;
D; Mismatches
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                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                            Dietrich, N., Dubuque, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>,</u>
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227 60

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REFERENCE
AUTHORS
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VERSION
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AI785039
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Best Local S
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 380)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Waterston, R. and Wilson, R.

Waterston, R. and Wilson, R.

Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                            ui73a06.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1888018 5' similar to gb:X81579 M.musculus mRNA for
insulin-like growth factor binding (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                    AI785039
AI785039.1 GI:5332755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4444 Forest Park Parkway, Box 8501,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: custom primer used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGI:971987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCCAGAGAGCTGTGACCACCACCTTCCGCTACTAGCTA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGTCCACTGCCCGACGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGTCCACTGCCCGCGGAGACACACCCAGCGAGCATTGAACACTGCACACGGTCGTCT
                                                                                                                                                                                                                                                                   musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 420.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Sugano mouse liver mlia"
//clone_lib="Sugano mouse liver mlia"
//note="Organ: liver; Vector: pMBL8S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); lst Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments of.1skb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
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Pred. No. 1.1e-14;
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Search completed: September

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Best Local Similarity
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                                                231 CAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 265
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other_ESTs: ui73a06.x1
                                                                                                      TCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCATACGGCCGTCTGCC
CAGAGAGCTGTGACCACCATTGCCACTACTATCTA
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                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                 /Clone_lib="Sugano mouse liver mlia"
//Clone_lib="Sugano mouse liver; Metles-FL3; Site_1: DraIII
//Clone_Torgan: liver; Vector: pMELBS-FL3; Site_1: DraIII
(CACCTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pMElBS-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop:
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lab_host="DH10B"
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/strain="C57BL"
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clone="IMAGE:1888018"
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Pred. No. 8.3e-14;
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pubpna/US07_
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| Cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO7_NEW PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO7_NEW PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO09_PUBCOMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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/cgn2_6/ptodata/2/pubpna/US11 NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US11 NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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US-09-972-916A-6

US-09-972-916A-4

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                    Sequence 3, Appli
Sequence 6, Appli
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US-10-363-345A-40493	-10-087-192-39	2-122A-332	-10-425-115-28	-10-367-094-1	-09-764-872-58	-10-072-012-	-10-120-988-	-10-292-798-	-017-161-	-10-343-903-	10-322-281-4	10-437-963-7918	US-10-437-963-79162	10-108-260A-223	10-250-615-	10-741-600-	10-741-601-	10-011-585/	US-10-027-632-164336	10-027-632-16433	US-10-739-930-	US-10-027-632-1749	US-10-027-632-17496	US-10-085-117-1	US-10-221-613-	US-10-311-455-970	US-10-152-319A-	US-10-388-934-3	US-09-972-916A	US-09-972-91	US-09-972-916 <i>F</i>	US-10-893-315	US-10-893-315	US-10-756-149	US-09-880-107-2393	US-10-152-319A-	US-10-191-80
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ALIGNMENTS

RESULT 1 US-09-972-916A-3

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                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 3
LENGTH: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09972916A
Patent No. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
                                                                                                                                                 Query Match
Best Local (
                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/972,916A CURRENT FILING DATE: 2001-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION FILE REFERENCE: US 1292/01 (VA)
                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                           / Match 100.0%;
Local Similarity 100.0%;
hes 270; Conservative 0
  61 AAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCGT 120
                                                                    1 CATGGGCGCACGGGGCACTCCCCGTGGTTCCTGGACTCTGGCCCCCCAGTGTATCACAAGCA 60
                                       CATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTATCACAAGCA 60
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Pred. No. 3.2e-86;
); Mismatches 0;
                                                                                                                                                                  Length 270;
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Sequence 6, Application US/09972916A

Patent No. US20020107198A1

GENERAL INFORMATION:
APPLICANT: Thule, Peter M.

TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A

CURRENT FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/239,113

PRIOR APPLICATION NUMBER: US 60/239,113

PRIOR FILING DATE: 2000-10-11

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 6

LENGTH: 423
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                                                                                     Sequence 4, Application US/09972916A Patent No. US20020107198A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
              APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
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ORGANISM: Artificial Sequence
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tive 0; Mismatches 0;
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Sequence 5, Application US/09972916A
Patent No. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
FILE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INS
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 5
LENGTH: 372
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US-09-972-916A-5
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NUMBER OF SEQ ID NOS: 6
SEQ ID NO 4
                                                                                                                                                                                                                              Best Local Similarity Matches 220; Conserv
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Best Local &
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Best Local Similarity
Matches 220; Conserv
                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION: Synthesized
332
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                                                                                 GTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACGCCCATCTGC 229
                                                                                                               GTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGC 229
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                         CCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC 270
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Pred. No. 4.7e-68;
0; Mismatches 1
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372
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PRIOR APPLICATION NUMBER: US 60/22,040
PRIOR FILLING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/22,880
PRIOR FILLING DATE: 2000-11-02
PRIOR PELLONG DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR PILLING DATE: 2001-05-11
PRIOR PELLORATION NUMBER: US 60/290,645
PRIOR FILLING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILLING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILLING DATE: 2001-06-19
PRIOR FILLING DATE: 2001-06-19
PRIOR FILLING DATE: 2001-06-19
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Patent No. US20020107198A1

GENERAL INFORMATION:
APPLICANT: ThuLe, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1992/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
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SEQ ID NO 2
LENGTH: 219
TYPE: DNA
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Best Local Similarity
Matches 219; Conserv
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                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Blashoff, Michael
APPLICANT: Blashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44291-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-3
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; PRIOR FILING DATE: 2001-07-09; NUMBER OF SEQ ID NOS: 1740; SOFTWARE: PATENTIN Ver. 2.1; SEQ ID NO 1608; LENGTH: 1500; TYPE: DNA
RESULT 8
US-10-191-803-73
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                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 21199
CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 02005336.9
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
SOFTWARE: Patentin version 3.1
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Publication No. US20
GENERAL INFORMATION:
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Best Local
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APPLICANT: Suter-Dick, Laura
APPLICANT: Wolf, Detlef
TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
FILE REFERENCE: 21199
                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Rattus norvegicus (No. US20040005547Alway rat)
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ORGANISM: Rattus norvegicus
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                                                                                                                                                                                                                 28.3%;
Local Similarity 98.7%;
es 77; Conservarion
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                                                                          68 CACTTCCGCTACTATCTA 85
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No. US20040005547A1
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98.7%;
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Pred. No. 1.5e-16;
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                                                                                                                                                                                                                          Indels
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Sequence 73, Application US/10191803
Publication No. US20040014040A1
GENERAL INFORMATION:
APPLICANT: MENDRICK, Donna
APPLICANT: PORTER, Mark
APPLICANT: JOHNSON, Kory
APPLICANT: HIGGS, Brandon
APPLICANT: CASTLE, Arthur
APPLICANT: ELASHOFF, Michael
TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling

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CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,819
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/305,623
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: US 60/377,611
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 1140
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Publication No. US20040072160A1
SEQ ID
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LENGTH: 1500
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PRIOR
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TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR FILING DATE: 2001-05-22
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR
PRIOR
                                      Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 2221
                                                                                  PRIOR APPLICATION NUMBER: US 60/330,462 PRIOR FILING DATE: 2001-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mendrick, Donna
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_013144
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                                                                                                                       OR APPLICATION NUMBER: US 60/303,807
OR FILING DATE: 2001-07-10
OR PILING DATE: 2001-07-10
OR APPLICATION NUMBER: US 60/303,808
OR FILING DATE: 2001-07-10
OR APPLICATION NUMBER: US 60/315,047
OR FILING DATE: 2001-08-28
OR APPLICATION NUMBER: US 60/324,928
OR APPLICATION NUMBER: US 60/324,928
OR FILING DATE: 2001-09-27
OR APPLICATION NUMBER: US 60/330,867
OR FILING DATE: 2001-11-01
OR FILING DATE: 2001-11-01
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FILING DATE: 2001-06-13
APPLICATION NUMBER: US 60/298,925
FILING DATE: 2001-06-19
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/303,810 FILING DATE: 2001-07-10
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                      PatentIn Ver.
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Higgs, Brandon
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Pred. No. 1.5e
0; Mismatches
                                                             See File Wrapper or PALM
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US-09-880-107-2393
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US-09-880-107-2393
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SEQ ID NO 2393
LENGTH: 6128
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APPLICANT: Vockley
APPLICANT: Scherf,
APPLICANT: Gene Lo
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Best Local
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NUMBER OF SEQ ID NOS: 3950
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TITLE OF INVENTION: Gene Expression Profiles
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TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. NM_013144
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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645
                                                                     593 GAGCATCGGCCACCGCCATCC-----CATCCAGCGAGCATCTGCCGCCGCCGCCGC
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                                                                                                       163 CAGCATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGC-ACACGG
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                    CCATCTGCCCAGAGAGCTGTGACCACCACTTC
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CCACCCTCCCAGAGAGCACTGGCCACCGCTCC
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Scherf, Uwe
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98.7%;
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Pred. No. 8.9e-11;
0; Mismatches 52;
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Pred. No. 1.5e-16;
); Mismatches 1
676
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RESULT 11 US-10-756-149-1484

Sequence 1484, Application US/10756149 Publication No. US20050181375A1

GENERAL INFORMATION:

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; ORGANISM: Human
US-10-893-315-126
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US-10-893-315-126
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; ORGANISM: Homo Sapiens
US-10-756-149-1484
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Publication No. US20050147987A1
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000786
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 2172
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 126
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CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1484
LENGTH: 6128
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Best Local
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Best Local Similarity 66.5%;
Matches 141; Conservative
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CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: 60/231,397
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TITLE OF INVENTION: MOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Aziz, Natasha
APPLICANT: Zlotnik, Alb
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                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                     1877
1997
                                  163
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                      CAGCATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGC-ACACGG
                                                                                                  TAACCC-----GTGCTGCCGAGCCAGCCCTTCATAAGGCCCCTGGGTATGGCCAGC
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                                                                       TAACCTCCTGGTGCAAGTGGCGCGGCCTGTGCCCCTTTATAAGGTGCGCGCTGTGTCCAGC
                                                                                                                                                     CACTAGCAAAACTTATTTTGAACACTCAGCTCCTAGCGTGCGGCGCTGCCAATCAT
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Pred. No. 1e-10;
0; Mismatches 52;
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Pred. No. 8.9e-11;
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GENERAL INFORMATION:
APPLICANT: Thile, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF IN:
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LENGTH: 9174
; TYPE: DNA
; ORGANISM: Human
US-10-893-315-160
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US-09-972-916A-1
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09972916A Patent No. US20020107198A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 160
                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 141;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000786
CURRENT APPLICATION NUMBER: US/10/893,315
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 2172
NUMBER OF SEQ ID NOS: 2172
                                                                                                                 TYPE: DNA
ORGANISM: Rattus
                                                                                                       FEATURE:
                                                                                                                                                            LENGTH: 51
Local Similarity
nes 51; Conserv
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                 18.9%; Score 51; DB 9; L
100.0%; Pred. No. 6.4e-08;
0;
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Mismatches
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                                    Length 51;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Match Length
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270 .
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    1202784 seqs, 818138359 residues
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Copyright (c) 1993 - 2005
    , Gapext 1.0
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           US-09-949-001-36
US-08-945-140-1
US-08-945-140-1
US-08-949-016-11786
US-09-949-016-12194
US-09-949-016-73784
US-09-949-016-73895
US-09-949-016-13895
US-09-949-016-13895
US-09-949-016-11816
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US-09-949-016-115518
US-09-949-016-115518
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US-09-949-016-11590
US-09-949-016-1159693
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Sequence 30, Appl Sequence 1, Appli Sequence 1, Appli Sequence 11786, A Sequence 11786, A Sequence 1725, Appli Sequence 2153, Appli Sequence 2153, Appli Sequence 3, Appli Sequence 3, Appli Sequence 11745, A Sequence 11745, A Sequence 11745, A Sequence 1615, A Sequence 1615, A Sequence 1616, A Sequence 1616, A Sequence 16518, A Sequence 16590, A Sequence 16590, A Sequence 16992, Sequence 16992, Sequence 11990, A Sequence 11990, A Sequence 11990, A Sequence 1518, Ap Sequence 13109, A Sequence 13109, A Sequence 1341, Ap Sequence 1381, Ap Sequence 3891, Ap Sequence 3891, Ap Sequence 3891, Ap Sequence 4025, Ap
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RESULT 2 US-09-949-001-36

Sequence 36, Application US/09949001
Patent No. 6925336
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION

DETECTION AND USES THEREOF

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2049

CCATCTGCCCAGAGAGCTGTGACCACCACTTC 253

1997 222

163

2048

Qy 113 T	Qy 53 C Db 1877 C	Query Match Best Local Si Matches 141;	RESULT 1 US-09-949-001-30 Sequence 30, Application US/099490 Patent No. 6825346 GENERAL INFORMATION: APPLICANT: VENTER, J. Craig et al TITLE OF INVENTION: POLYMORPHISMS; TITLE OF INVENTION: WITH OSTEOPE FILE REFERENCE: CL000789 CURRENT APPLICATION NUMBER: US/09 CURRENT FILING DATE: 2003-01-15 CURRENT FILING DATE: 2003-01-15 PRIOR APPLICATION NUMBER: 60/231, PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 848 SOFTWARE: FastSEQ for Windows Ver SEQ ID NO 30 LENGTH: 9173 TYPE: DNA ORGANISM: Human US-09-949-001-30		45 28.8	4 28.	43 28.	41 29	. 20	N	3 37	N	35 29.	34 29.	32 29.	31 30.	c 30 30.6	28 30.
TAACCC TAACCTCCTGG	ACAAGCAAA ACTAGCAAA	Similarity Siconserva			10.7	•		٠.	. 7	. 7		. 7	80		ò	N	11.3 2	
GTG GTGCAAGTG	ACAAACTTA ACAAACTTA	22.5%; 66.5%; tive	ion US/09949001 Craig et al. POLYMORPHISMS I WITH OSTEOPORO 10789 NUMBER: US/09/9 2003-01-15 7MBER: 60/231,32 000-09-08 i: 848 ir Windows Versi		1383 1	7 4	ωı		4.	.44	4, 4	ω	4.		· w	4.	93 4	υ c 4.4
TAACCCGTGCTGCCGAGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAGC	CACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCAT	Score 60.8; DB 4; Len Pred. No. 3.7e-10; 0; Mismatches 52; In	O1 IN KNOWN GENES ROSIS, METHODS /949,001 323 Sion 4.0	ALIGNMENTS	US-08-484-044-1	US-09-902-540-3367	US-09-067-782A-3	US-07-642-734C-3	US-09-949-016-15911	US-09-252-991A-11038	US-09-270-767-10411	US-08-998-416-479	US-09-205-258-119	US-09-621-976-2783	US-09-067-782A-1	-910	US-09-902-540-1241	09-252-991A-39
CCCTGGGTATGO	GCTGCCCTGACA	Length 9173; Indels 19;	OF DETECTION AND U				Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence
3CCAGC 162 CCAGC 1996	NATCAT 112 NATCAT 1936	Gaps 3;	USES THEREOF		1, Appli	3367, Ap	3. Appli		15911	11038	10411, A	479,	119,	1783, Ap	1, Appli	17016, A	1241, Ap	3919, Ap

FILE REFERENCE: CL000789

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PRIOR APPLICATION NUMBER: 60/231,323
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FASTSEQ for Windows Version 4.
SEQ ID NO 36
LENGTH: 9174
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; ORGANISM: Human
US-09-949-001-36
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GENERAL INFORMATION:
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Best Local Similarity
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CURRENT FILING DATE: 2003-01-15
                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,140
NAME: Savitzky Esq., Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: EX95002-US
TELECOMMUNICATION INFORMATION:
                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/04558
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR96,
FILING DATE: 12-APR-1996
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: GLUCOSE-INDUCIBLE RECOMBINANT VIRAL TITLE OF INVENTION: VECTOR NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CHEN, Ruih
APPLICANT: DOIRON, Br
APPLICANT: KAHN, Axel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 19426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 500 Arcola Road, Mailstop 3C43 CITY: Collegeville
                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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Pred. No. 3.7e-10;
0; Mismatches 52;
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RESULT 4
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GENERAL INFORMATION:
APPLICANT: Makoto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 18.9%; Sometime 18.0%; East Local Similarity 100.0%; Education 10.0%; Education 10.0%; Matches 51; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1-
SEQUENCE CHARACTERISTICS:
LENGTH: 13011 base pairs
TYPE: nucleic acid
                                                                                       ORGANISM:
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatibl
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                   FEATURE:
NAME/KEY:
                                                                                                                                                          ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 805 Fift
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/791,849A FILING DATE: January 30, 1997
                                                      LOCATION:
                                                                      LOCATION:
                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Makoto MURASE et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (610) 454-3808
                                                  join(3212..3218, 3766..3948, 5917..6008, 6152..6283, 6418..6604, 6921..7191, 7302 9298..9479, 10163..10269)
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exon
join(3194..3218, 3766..3948, 5917..6008.
                                                                                                         CDS
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                                                                                                                                         rat (Rattus norvegicus)
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                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                double
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Pred. No.
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                                                                      7302..7452, 7665..7817, 7911..8077
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OCATION:

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US-09-949-016-11786
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                                                       CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-10-08
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                   SOFTWARE: Fast
                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: VENTER, J.
                                                                                                                                                                                                                                                                                                                    Patent No. 681233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICATION: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                             TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS FILE REFERENCE: CLOO1307
CURRENT ADDITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 51; Conservative
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Best Local S
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
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NAME/KEY:
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LOCATION:
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                                          FastSEQ for Windows Version 4.0
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6284..6417, 6605..6920, 7191..7301, 7453..7664, 7818..7910,
9480..10162)
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Pred. No. 0.09
0; Mismatches
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Pred. No.
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1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .096;
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OF DETECTION
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US-09-949-016-73784/c
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US-09-949-016-17205
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                                                                                                                                                                                                                                                       Sequence 73784, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows
SEQ ID NO 19194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 39; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-9-08
PRIOR FILING DATE: 2000-9-08
PRIOR FILING DATE: 2000-9-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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55.3%;
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9 CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 51 CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCTGGCATA 2399 Score 36.6; DB (Pred. No. 0.096; 4 Length 15108; 0 Gaps

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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FALLIGATION NUMBER: US/09/949,016
CURRENT FILLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PRIOR PAPLICATION NUMBER: 60/241,756
PRIOR FILING DATE: 2000-10-20
PRIOR PRIOR DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PRIOR APPLICATION NUMBER: 60/231,498 CCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACA 189 CCAGGCCTTCCTGGGGCGCTGTTCCTCTCCATCCAGCTTAGCCACCTGCCAGGTTAGGCC Score 35; DB 4; Pred. No. 0.075; 0; Mismatches 5 55; Indels 0 Gaps 419

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14 190 CANACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCACCA 249 CCCATCCAGAGACACACCCCGGATCACAGCCCTGCCACCACCACCACTCCATGCATAGCC

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US-09-949-016-2153/c
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; ORGANISM: Human
US-09-949-016-73784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
Sequence 74, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2153
LENGTH: 2393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Human
-09-949-016-2153
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Best Local Similarity
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                                                                                                                                                                                                                                                           2122
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                                                                                                                                                                                    CTT 2060
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55.3%;
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Pred. No. 0.14;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 2393;
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OF DETECTION AND USES THEREOF
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; ORGANISM: Human
US-09-949-016-11816
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US-09-949-016-11816/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR OF SEQ ID NOS: 207012
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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Matches
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS

FILE REFERENCE: CLOO1307

CURRENT APPLICATION UNMEER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11816
LENGTH: 7561
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Best Local Similarity
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ORGANISM: Human
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nes 68; Conserv
                                                                 5290 CCCATCCAGAGACACATCCACCCGGATCACAGCCCTGCCACCACCACTCCATGCATAGCC 523
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ilarity 55.3%;
Conservative
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Pred. No. 0.25;
0; Mismatches 5
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Pred. No. 0.14;
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Best Local Similarity 55.3
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Patent No. 5856454
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SEQ ID NO 13895
LENGTH: 7562
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                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PLOAME: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: 09
APPLICATION NUMBER: US/08/304,309
PILING DATE: 09-SEP-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                           ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GONZALEZ, Frank J.

APPLICANT: FERNANDEZ-SALGUERO, Pedro
TITLE OF INVENTION: CLONING AND EXPRESSION OF CDNA FOR HUMAN
TITLE OF INVENTION: DIHYDROPYRIMIDINE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                            STREET: Steuart Stre
CITY: San Francisco
                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                           California
                                                                                                                                                                                                                                                                                                                   Steuart Street Tower,
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55.3%;
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Pred. No. 0.25;
0; Mismatches
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US-08-991-942-3
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/304,309
FILING DATE: 09-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 15280-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                             ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FERNANDEZ-SALGUERO, Pedro
TITLE OF INVENTION: CLONING AND EXPRESSION OF CDNA FOR HUMAN
TITLE OF INVENTION: DIHYDROPYRIMIDINE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                           APPLICATION NUMBER: US/08/991,942 FILING DATE:
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LOCATION:
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                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
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88..3162
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Pred. No. 1.8;
0; Mismatches
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TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 4447 base pairs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-09-949-016-11745
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                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING NUMBER: 60/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/337,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/331,498
PRIOR FILING DATE: 2000-09-08
NIMBER DE ESO. 10 NOS. 2000-09-08
NIMBER DE ESO. 10 NOS. 2000-09-08
                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Best Local Similarity
Matches 82; Conserv
                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11745, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 207012
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NAME/KEY:
LOCATION:
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NAME/KEY: misc_feature
LOCATION: 1.4447
OTHER INFORMATION: /product= "Pig_DPD"
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                            2395 ATCAGACCAATTGCTTTGAGAGCTGTGACCACCATTGCTCGTGCT 2439
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                                                      GCAGGGTTCACTCGAGGCCAAGCCATGGCCACTGGCCCCAGGGGAGAATCCCCTTGTTTC 2771
                                                                                        GCATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCA 224
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milarity 53.1%;
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88..3162
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 Length 4447;

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Search completed: September Job time: 87.4384 secs 1, 2005, 07:07:09

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Result
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Maximum DB
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Perfect score:
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 1188.8
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Match Length
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Listing first 45 su
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BC013345
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Compugen Ltd.
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                                     AX163782 Sequence
L22979 Rat insulin
BC078889 Rattus no
AY095345 Papio anu
AX409747 Sequence
                                                                            AC136382 Rattus no
X67493 M.musculus
AL607124 Mouse DNA
BC011345 Mus muscu
AY560836 Sepumophi
AX401932 Sequence
AX827271 Sequence
AX827271 Sequence
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M59316 Human insul
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ALIGNMENTS

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REFERENCE
AUTHORS
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RATILGFZ
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Best Local Similarity
Matches 218; Conserv
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                213
                                             873
                                                                                                     813
                                                                                                                                  93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        insulin-like growth factor.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RATILGFZ 1181 bg
Rattus norvegicus insulin-like
M84484
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Mammalia; Eutheria;
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CCAGCATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGG
                                          CTGACAATCATTAACCCGTGCCGAGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAG 212
                                                                                                     TGTGCGGAGCTCACAAGCAAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCC
                                                                                                                      TGCGCCCATGTCACAAGCAAAACCAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCC 152
                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 1181)
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="Sprague-Dawley"
/db xref="taxon:10116"
/sex="male" "live"
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                 /tissue_type="liver"
/dev_stage="adult"
                                                                                                                                                                          66.8%;
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Rodentia;
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Pred. No. 4.6e-53;
0; Mismatches 6
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er gene fragment.
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  AUTHORS
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                                                                                      Bryant, N., Blant, V., Blankenbuldy, N., Bryth, P., Center, R., Chen, S., Chen, S., Chen, R., Chen, Z., Chu, J., Charderon, S., Chen, R., Chen, R., Chen, Z., Chu, J., Charderon, S., Davila, M.L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Duysis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Denn, A., Durbin, K., Daval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Escotto, M., Hernandez, J., Evans, C.A., Falls, T., Fan, G., Egan, A., Escotto, M., Hernandez, J., Gunaratine, P., Haalland, M., Hamil, C., Hamilton, C., Hamilton, K., Harrey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hellins, S., Hulyk, S., Hune, J., Idebird, D., Jackson, A., Jakkson, A., Jan, R., Lu, J., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Ben. Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardens, V., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardens, V., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardens, V., Cardens, V.,
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Allen,C., Allen,H., Alsbrooks,S.
Anyalebechi,V., Aoyagi,A., Ayode
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                                                   Unpublished
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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tus norvegicus clone CH230-97018,
, 63 unordered pieces.
36382
  Genome Sequencing Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baylor Plaza, Houston, TX 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.h NOTE: This is a 'working draft' sequence. It currently consists of 63 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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Consensus quality: 135613 bases at least Q40
Consensus quality: 140849 bases at least Q30
Consensus quality: 145680 bases at least Q20
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661032: gap of unknown 1
66045: contig of 1983 b
661132: gap of unknown 1
66045: contig of 3003 b
68197: contig of 3003 b
68297: gap of unknown 1
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78303: gap of unknown 1
78403: contig of 3468 b
72335: contig of 3468 b
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84673: contig of 3003 b
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101618: contig of 3788 b
98830: gap of unknown 1
101618: contig of 3798 b
101718: gap of unknown 1
105635: gap of unknown 1
1056364: gap of unknown 1
1056364: gap of unknown 1
113664: gap of unknown 1
126644: contig of 3798 b
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122602: contig of 4071 b
122602: contig of 4072 b
1226044: gap of unknown 1
126644: contig of 4042 b
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2 (bases 1 to 1363)

2 (bases 1 to 1363)

Nohn, K. L., Waddle, J. R. and Taub, R.

Comparison of mouse and human IGFBP-1 genes reveals a potential

Comparison of mouse and conservation of all intron/exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (23-JUL-1992) R.A. Taub, Univ. of Pennsylvania, Hughes Medical Institute, Clinical Research Bldg., Room 4. Curie Boulevard, Philadelphia, PA 19104-6145, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mohn.K.L., Bucan,M. and Taub,R.

Structure and localization of the IGFBP-1 gene and its expression during liver regeneration
Hepatology 19 (3), 656-665 (1994)
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insulin-like growth factor binding protein-1.
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Mus musculus
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1363)
Lee,J., Greenbaum,L., Haber,B.A., Nagle,D., Lee,V., Miles,V.,
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                                                                                                                                                                                                                                                                                                                                             /cell_type="fibroblast"
/clone_lib="genomic, lamb
/dev_stage="embryo"
500._508
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="genomic DNA"
/strains"NIH Swiss"
/db_xref="taxon:10090"
/clone="VW2.1"
/cell_line="NIH 3T3"
/cell_type="fibroblast"
/product="insulin-like growth factor
/protein id="CAA47832.1"
/db_xref="GI:52700"
/db_xref="GOA:P47876"
/db_xref="UniProt/Swiss-Prot:P47876"
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                                                                            source
                                                                                                                                                                                                                                                                                                                                                            Cambridgeshire, CBIO 1SA, UK. E-mail enquiries:
humquery@aanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 12, 2002 this sequence version replaced gi:19847866.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
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                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-20C9 from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                            assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                               database can be found at
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Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse DNA sequence from clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL607124.15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCATCTGCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGCATGGTCCACTGCCCGCCGAGAGACACAAACCCAGCGAGCATTGAACACTGCACACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGACAATCATTAACCTGTGCCGCACAGCCAGCCCTTCATAAGGCTCTGGGTACGACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGACAATCATTAACCCGTGCTGCCGAGCCAGCCCTTCATAAGGCCCCTGGGTATGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCGCCCATGTCACAAGCAAACAAACTTATTTTGAACACGGGGGATCCTAGCACGCTGCC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGTCTGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
/organism="Mus musculus'
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MPEFLTVVSWPFLILLSFQIGVAAGAPQPWHCAPCTAERLGLCPPVPASCPEISRPAGCGCCPTCALPMGAACGVATARCAQGLSCRALPGEPRPLHALTRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGASLPEPAAPATSTLFSSQHE"
                                                                                                   Location/Qualifiers
                                                                            .192843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:20145926
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Pred. No. 2.1e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RP23-20C9 on chromosome
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BC013345
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                                                                                                                                                                                                                                                                                                                                                                                                    RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Parmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunarathe, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Wadan, A., Kodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2539
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                         Direct Submission
Submitted (31-AUG-2001) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC013345 1569 bp mRNA linear ROD Mus musculus insulin-like growth factor binding protein (cDNA clone MGC:14075 IMAGE:4161889), complete cds.
                                                                                                       Contact: MGC help desk
                                                                                                                                                                                   Gene Collection (MGC), Cancer Genomics Office, National Institute, 31 Center Drive, Room 11AO3, Bethesda, MD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih
                                                                                                                                                                                                                                                                                          Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                 human and mouse cDNA sequences
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/clone_lib="RPCI-23"
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Pred. No. 2.
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Li,Y., Klimanis,D. and Hallenbeck,J.M.
Cloning and characterization of insulin-like growth factor binding protein 1 (IGFBP-1) from thirteen-lined ground squirrel
                                                                                                                                                                                              AY560836 1507 k
Spermophilus tridecemlineatus
protein 1 (IGFBP1) mRNA, compl
AY560836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 18 Row: i Column: 20
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Similarity but not identity to protein.
                                                                                                                          Spermophilus tridecemlineatus (thirteen-lined ground squirrel) Spermophilus tridecemlineatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                AY560836.1 GI:45505308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be
                                                                       Spermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                              CACACGGCCATCTGCCCAGAGAGAGCTGTGACCACCACCTTCCGCTACCTAGCTA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTG
                                                                                                                                                                                                                                                                                                                                        CACACGGCCGTCTGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 130
                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 1507)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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PVPASCPEISRPAGCGCCPTCALPMGAACGVATARCAQGLSCRALPGEPRPLHALTRG
QGACVPEPAAPATSTLSSQHEEAKAAVVSADELSESPEMTERGLLDSFHLMAPSRED
QFILMNAISTYSSMAAREIADLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNKNGFYHSKQCETSLDGEAGLCWCVYPWSGKKIPGSLETRGDPNCHQYFNVHN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="insulin-like growth factor binding 
/protein id="AAH13345.1" 
/db xref="GI:15426483" 
/db xref="LocusID:16006" 
/db xref="MGI:96436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="synonym: IGFBP-1"
/db_xref="LocusID:16006"
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/clone="MGC:14075 IMAGE:4161889"
/tissue_type="Liver, normal. 5 mv
/clone_Tib="WCI_CAP_Li9"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="MGI:96436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="Vector: pCMV-SPORT6"
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Pred. No. 2.7e-18;
0; Mismatches 8;
                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Sciuridae; Sciurinae;
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Local Similarity
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Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                              AX401932 1500 bp
Sequence 1608 from Patent WO0210453
AX401932
                                                                                                                                                         Patent:
                                                                                                                                                                                               Elashoff, M.R.
                                                                                                                                                                                                                      Mendrick, D.,
                                                                                                                                                                                                                                                                                                                                                                                            AX401932.1 GI:21338112
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                                                                                                                                                                        Molecular toxicology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCGCCCATGTCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCC
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                                                                                                                                                  WO 0210453-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MPEVPAAGLWPFILLLAVQVSTVASSTQPWHCAPCSAEKLALCP EVPSSCPELSRPAGCGCCPMCALPLGAACGVATARYARGLSCRALPGEPRFLHALTRG QGACVPEPATPTASGLSS I EKEEAKASMVPBRVPPESAEMTEEQLLESFHLMASSSED QPILWWAISTYKSMRAREWADIKKWKQPCRRELYKVLERLAKAQQKAGSEIYKFYLDW CNKNGFYHSKQCETSLDGEAELCWCVYPWSGRRIPGSLEIRGDPNCHQYFNVQN"
                                                                                   Location/Qualifiers
                    organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
note="EMBL/GenBank Accession No. NM_013144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/product="insulin-like
/protein_id="AAS67029.1
/db_xref="GI:45505309"
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organism="Spermophilus"
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                                                                                                                                                                                                                 Porter, M.W.,
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67.1%;
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Pred. No. 1.3e-12;
0; Mismatches 58;
                                                                                                                                                                                                                 Johnson, K.R.,
                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
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RATIGFB
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Best Local S
Matches 77
                                                                  MEDLINE
PUBMED
                                                                                                                        AUTHORS
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TITLE
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                                                                                                                                                                                                   RATIGFB 1500 bp
Rat IGF binding protein-1 (rIGFB M58634 M58634.1 GI:204732
IGF binding protein-1 Rattus norvegicus (Norway rat)
Rattus norvegicus
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Methods f
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                                                                                           Mohn, K.L., Melby, A.E., Tewari, D.S., Laz, T.M. and Taub, R
The gene encoding rat insulinlike growth factor-binding
is rapidly and highly induced in regenerating liver
mol. Cell. Biol. 11 (3), 1393-1401 (1991)
                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AX827271
Sequence 5 from Patent I
AX827271
AX827271.1 GI:39837360
                                                    Original
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                 Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ess,F., Suter-Dick,L. and Wolf,D. thods for the toxicity prediction tent: EP 1344834-A 5 17-SEP-2003; HOFMANN-LA ROCHE AG (CH)
Location/Qualifiers
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                                                       source text: Rat, cDNA to
1. .1500
/organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from Patent EP1344834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.8%;
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98.7%;
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Rodentia;
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Pred. No. 8.9e-12;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 76.4; DB 6;
Pred. No. 8.9e-12;
D; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1500
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1 (rIGFBP-1) mRNA,
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Sciurognathi; Muridae;
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                                                                                                                                                                               Euteleostomi; 
Murinae;
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; Murinae;
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AX163782
                                                             ۲
                                                                                                                          Similarity
                                                                                                                                                                                                                                                                             Method of identifying toxic agents ugene expression in liver Patent: WO 0138579-A 46 31-MAY-2001; Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Norway Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                            Gould-Rothberg, B.E., Dipippo, V.A.,
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                                                                           CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCCAGAGAGCCTGTGACCAC
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 CACTTCCGCTACTATCTA
                             CACTICCGCTACTAGCTA 316
                                                             CACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCCAGAGAGCTGTGACCAC
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                                                                                                                        Conservative
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235. .975
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46 from Patent WO0138579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MPEFLTVVSWPFLILLSPQVRVVAGAPQPWHCAPCTAERLELCP pVPASCPEISRPAGCGCCFTCALPLCAACGVATARCAGGLSCRALPGEBRPLHALTRG OGACVLEPAAPATSSLSGSQHEEAKAAVASEDELAESPEMTEEQLLDSFHLMAPSRED OGACVLEPAAPATSSLTDLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN QRINMAISTYSSMRAREITDLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN CNKNGFYHSKQCETSLDGEAGLCWCVYPWSGKKIPGSLETRGDPNCHQYFNVQN"
                                                                                                                                                                                               /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="IGF binding protein-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="IGF binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="Fisher"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:10116"
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98.7%;
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Rodentia;
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                                                                                                                        Score 76.4; DB 6;
Pred. No. 9.5e-12;
D; Mismatches 1;
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Pred. No. 8.9e-12;
D; Mismatches 1
                                                                                                                                                                                                                                                                                                                        o,V.A., Ramseh,T.M. and Gerwein,R.W.
agents using nsaid-induced differential
                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
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RESULT 11 RATIGFBA

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Best Local Similarity
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239 CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
                                                      77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Norway rat)
Rattus norvegicus
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Nov 30, 1995 this sequence version replaced gi:385167 Original source text: Rattus norvegicus (strain Sprague-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dideoxy sequencing and structural analysis of growth factor binding protein-1 gene Biochim. Biophys. Acta 1218 (1), 95-98 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lacson, R., Oehler, D., Yang, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             insulin-like growth factor binding protein-1
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                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   PVPASCPEISRPÄGCGCCPTCALPLGAACGVATÄACAQGLSCRALPGEPRPLHALTRG
QGACVLEPAAPATSSLSGSQHEEAKAAVASEDELAESPEMTEEQLLDSFHLMAPSRED
QPILMNAISTYSSMRAREITDLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
                                                                                                                                                                                            3003. .4089
/gene="IGFBP-1"
                                                                                                                                                                                                                                                                                                                                                                                                                    CNKNGFYHSKOCETSLDGEAGLCWCVYPWSGKKIPGSLETRGDPNCHQYFNVQN"
                                                                                                                                                                                                                                                                                          2035. .2873
/gene="IGFBP-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/product="insulin-like growth factor binding protein"
/protein id="AAA82581.1"
/db_xref="GI:1098473"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="IGFBP-1"
join(153. .525,1850. .2034,2874. .3002,4090. .4221)
/gene="IGFBP-1"
                                                                                                                                                 number=4
                                                                                                                                                                              number=
                                                                                                                                                                                                                                           gene="IGFBP-1"
                                                                                                                                                                                                                                                                         number-2
                                                                                                                                                                                                                                                                                                                       number=2
                                                                                                                                                                                                                                                                                                                                        |850. .2034
|gene="IGFBP-1"
                                                                                                                                                                                                                                                                                                                                                                                      gene="IGFBP-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MPEFLTVVSWPFLILLSFQVRVVAGAPQPWHCAPCTAERLELCP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="liver"
dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       strain="Sprague-Dawley"
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                                                                23.8%;
98.7%;
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                                                   0,
                                               Score 76.4; DB 10;
Pred. No. 9.5e-12;
0; Mismatches 1;
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                                                                                Length 5001;
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PUBMED
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RS Straubberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,
Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,
Altschul, S. F., Zeeberg, B., Buctow, K. H., Schaefer, C. F., Bhat, N. K.,
Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,
Diatchenko, L., Warusins, K., Farmer, A. A., Rubin, G. M., Hong, L.,
Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,
Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,
Abramson, R. D., Millahy, S. J., Bosak, S. A., McEwan, P. J.,
McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S.,
McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S.,
Willalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Glbbs, R. A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y.,
Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,
Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M.,
Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 114 Row: e Column: 3:
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6981079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Director MGC Project.

Direct Submission

Submitted (02-NUG-2004) National Institutes of Health, Mammalian Submitted (02-NUG-2004) National Institutes Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.
Dickson, M., Schmutz, J., Grimwood, J., Rodri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus insulin-like growth factor binding protein 1, mRNA (cDNA clone MGC:93595 IMAGE:7129185), complete cds.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/organism="Rattus norvegicus"
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RESULT 13
AY095345
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Best Local Similarity
Matches 66; Conserv
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1 (bases to 386)

1 (bases to 386)

Kim,J.J., Taylor,H.S., Akbas,G.E., Foucher,I., Trembleau,A.,

Jaffe,R.C., Fazleabas,A.T. and Unterman,T.G.

Jaffe,R.C., Fazleabas,A.T. and Unterman, T.G.

Regulation of insulin-like growth factor binding protein-1 promoter activity by FKHR and HOXA10 in primate endometrial cells

7.71 Reprod. 68 (1), 24-30 (2003)
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                                                                                                                                Direct Submission
Submitted (11-APR-2002) Department of Obstetrics and Gynecology,
University of Illinois at Chicago, 820 S. Wood, Chicago, IL 60612,
                                                                                                                                                                                                                                                                                                                                                                                                          Papio anubis (olive baboon)
Papio anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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Papio anubis insulin-like growth factor binding protein-1 (IGFBP-1)
                                                                                                                            USA
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Kim, J.J., Jaffe, R.C. and Fazleabas, A.T.
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/protein_id="AAH78889.1"
/db_xref="GI:50927647"
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/db_xref="RATMAP:44422"
/db_xref="RGD:2872"
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/db_xref="LocusID:25685"
/db_xref="RATMAP:44422"
/db_xref="RGD:2872"
142. .960
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PVPASCPEISRPAGCGCCPTCALPLGARGVATARCAQCISCRADGEPRELHALTRG
QGACVLEPAAPATSSLSGSQHEEAKAAVASEDELASSPEMTEROLLDSFEHMAPSRED
QPILWNAISTYSSMRAREITDLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
                 /organism="Papio anubis"
/mol_type="genomic DNA"
/db_xref="taxon:9555"
                                                                                                    Location/Qualifiers
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/clone_Tib="NIH_MGC_236"
/lab_host="DH10B"
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Pred. No. 1.7e-08;
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                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2394 from Patent WO0229103. AX409747
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                    AX409747.1 GI:21442452
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ACACTCAGCTCCTAGCGTGCGGCGCGCCCAATCATTAACCTCCTGGTGCAAGTGGCGCGG
                    ACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCC------
                                                                      CACTTC 304
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/product="insulin-like
3655...>3886
/gene="IGFBP-1"
                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="unassigned DNA"
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                                                                                                                                                                                note="EMBL/GenBank Accession"
                                                                                                                                                                                                                                                  ocation/Qualifiers
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/db_xref="GI:20853765"
/translation="MSEVPVARYWLYLLLLTVQVGVTASAPWQCAPCSAEKLALCPPV
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                                                                                                                       Score 63.8; DB 6;
Pred. No. 5.6e-08;
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Pred. No. 4.8e-08;
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insulin-like growth factor binding protein.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Original source text: Homo sapiens (tissue library: lambda Charon4A) liver DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 6128)

Ehrenborg, E., Larsson, C., Stern, I., Janson, M., Powell, D.R. and
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Human insulin-like growth factor binding protein (hIGFBP1) gene,
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   TSMDGEAGLCWCVYPWNGKRIPGSPEIRGDPNCQMYFNVQN"
762. .836
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join(762. .1110,2657. .2826,4041. .4169,5069.
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/tissue_lib="lambda Charon4A"
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/map="7p13-p12"
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Perfect score:
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Copyright (c) 1993 - 2005
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gb_est2:
gb_est3:
gb_est5:
gb_est5:

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                                                    CV127049
CO560662
CO575629
CV117001
                                                                                                         AI790802
AI528304
AI196154
AI785039
CO573026
                                                                                                                                                                             AI529939
CA478518
                                                                                                                                                                                                      AI785818
AI196314
AI530146
AI098594
AI530313
               BB660958
CD561711
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Compugen Ltd.
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                                     BY783538 BY783538
BY78329 BY77317
A1785818 ui78h05.y
A1196314 ui71h07.y
A1530146 ui89f09.y
A1530146 ui89f09.y
A1530131 ui91601.y
A152939 ui87c09.y
CA478518 AGENCOURT
A1790802 uk28b10.y
A1528304 ui95g10.y
A1196154 ui69d08.y
A1196154 ui69d08.y
A1785039 ui773a06.y
CO573026 AGENCOURT
CV127049 AGENCOURT
CV127049 AGENCOURT
CO575629 AGENCOURT
              BB660958 BB660958
CD561711 B0435D02-
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36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.8	36.8	36.8	38.8	47.2	59	60.8	60.8	61.6	61.8	62.8	64.4	65.4	
11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.5	11.5	11.5	12.1	14.7	18.4	18.9	18.9	19.2	19.3	19.6	20.1	20.4	
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BX360059	CN402794	CD635412	CD635411	CN402792	CN402791	CN402790	CNS02Q6E	CV014020	BF829782	BU684425	AZ840793	AA060360	CR595377	CR621807	AW916227	BB604790	AA105355	CK473709	CK472246	75074004
BX360059	CN402794	CD635412	CD635411	CN402792	CN402791	CN402790	AL208895	CV014020	BF829782	BU684425	AZ840793	AA060360	CR595377	CR621807	AW916227	BB604790	AA105355	CK473709	CK472246	25071000
BX360059	170004240	56046444J	56046444H	170006000	170005321	170005319	Tetraodon	TL012B04	MR3-HN006	UI-CF-ENO	2M0138D02	mj67a12.r	full-leng	full-leng	EST347531	BB604790	mp37d09.r	AGENCOURT	AGENCOURT	T. OTBOOM

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Query Match
Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tlssue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9443 row: j column: 02
High quality sequence stop: 581.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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BF236974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF236974 1013 bp mRNA linear EST 14-NOV-2000 602026605F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4161889 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1013)
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                                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:4161889"
/lab_host="PHIOS (T1 phage-resistant)"
/clone_lib="NCI CGAP_Li9"
/clone_lib="NCI CGAP_Li9"
/note="Organ: liver; Vector: pCMV-SpORT6; Site_1: Not Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP_Library."
                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                      30.6%;
Score 98.2; DB 2;
Pred. No. 2.6e-17;
0; Mismatches 8;
                                              Length 1013;
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206 TGGCCAGCCATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTG

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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jag Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alzawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S., Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watahiki, A., Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A., Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K., Favan, W., Aidinis, V., Nakagawara, A., Held, M. A., Iwata, H., Kono, T., Nakauchi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M., Hensch, T.K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P., Muramatsu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y. Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia Genome Res. 13 (6B), 1273-1289 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Please visit our web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY783538 RIKEN full-length enriched, 17.5 days embryo Mus musculus cDNA clone L930176D05 5', mRNA sequence.
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                                                                                                                                                                                     Similarity
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TGCCCAGAGAGCTGTGACCACCACTTCCGCTACCTAGCTA 316
                                                                                                  ATGGTCCACTGCCCGCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATC
                                                                       ATGGTCCACTGCCCGCGGAGACACACACCCAGCGAGCATTGAACACTGCACACGCCCGTC
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                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                          tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="L930176D05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
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                                                                                                                                                                                   27.4%;
92.9%;
                                                                                                                                                             0;
                                                                                                                                                             Score 87.8; DB 6;
Pred. No. 2.1e-14;
0; Mismatches 7
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d, 17.5 days embryo whole body
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
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The Institute of Physical and Chemical Research (RIKEN)
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Carninci, P., Waki, K., Shiraki, T., Konno, H., Aizawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Sugahara, Y., Saito, R., Osato, N., Fukuda, S.,
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BY794229 RIKEN full-length enriched, 17.5 days embryo
Mus musculus cDNA clone L930292H24 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Res. 13 (6B), 1273-1289 (2003) 22703353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
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                                                                                                                                                                                                             Similarity
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TGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 100
                                                                                                                          ATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATC 277
                                            TGCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 316
                                                                                          ATGGTCCACTGCCCGCGGAGACACACACCCAGCGAGCATTGAACACTGCACACGCCCGTC 61
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                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       visit our web site (http://genome.gsc.riken.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                           /tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                  clone="L930292H24"
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                                                                                                                                                                                                                                                                                                                                                                                                                             db xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
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                                                                                                                                                                                                          Score 87.8; DB 6; Pred. No. 2.1e-14;
                                                                                                                                                                                       Mismatches
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d, 17.5 days embryo whole body
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RESULT 5
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1 (bases 1 to 354)

Carninci, P., Maki, K., Shiraki, T., Konno, H., Shibata, K., Itoh, M.,
Alzawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S.,
Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watahiki, A.,
Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A.,
Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K.,
Pavan, W., Aldinis, V., Nakagawara, A., Held, W. A., Iwata, H., Kono, T.,
Nakauchi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M.,
Nakauchi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M.,
Hensch, T.K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P.,
Muramatsu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y.
Targeting a complex transcriptome: the construction of the mouse
full-length cDNA encyclopedia
Genome Res. 13 (6B), 1273-1289 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                              218
                                                                                                                                                                                                                                         62
AI785818
401 bp mRNA linear EST 02-
ui178h05.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1888569 5' similar to gb:X81579 M.musculus mRNA for
insulin-like growth factor binding (MOUSE);, mRNA sequence
AI785818
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepare mouse tissues
Please visit our web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY771317.1 GI:39697955
EST.
Mus musculus (house mouse)
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354 bp mRNA linear EST 23-MAR-2
BY771317 RIKEN full-length enriched, 17.5 days embryo whole body
MUB_musculus cDNA clone L930052G15 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
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/db_xref="taxon:10090"
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92.9%;
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DEFINITION

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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Other_ESTs: ui78h05.xl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AI785818.1
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MGI:972893
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Fax: 314 286 1810
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//Clone_lib="Sugano mouse liver mlia"
//Clone="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
(CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st Strand cDNA
was primed with an oligo(dT) primer
[ATCTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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lab_host="DH10B"
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strain="C57BL"
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92.9%;
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Pred. No. 4.2e-14;
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KEYWORDS
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                                                                                 DEFINITION
                                                                                                                                                          RESULT 7
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AI530146
706 bp mRNA linear EST 18-MAR-19 ui89f09.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1889609 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This -----''' (info@mage.llnl.gov) for further information.
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
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Contact: Marra M/Mouse EST Project
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/note="Torgan: liver; Vector: pME18S-FL3; Site 1: DraIII
(CACTGTGTG); Site 2: DraIII (CACCATGTG); lst Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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Pred. No. 4.4e-14;
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AI530146
AI530146.1
            AI098594 765 bp mRNA linear kST zu-
ue31e07.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1481988 5' similar to gb:X81579 M.musculus mRNA for
insulin-like growth factor binding (MOUSE);, mRNA sequence.
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone ....'.-- 'i-f-Asimage.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
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The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 706)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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/strain="C57BL"
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            A1530313
785 bp mRNA linear EST 18-MAR-19 u191f01.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1889785 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
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Fax: 314 286 1810
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T. Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
The WashU-HHMI Mouse EST Project
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
sequence
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                                                                                                                                                                                                                                  GCCCAGAGAGCTGTGACCACCACTACTATCTA 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME185-FL3; Site 1: DraIII
(CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG] digested
and cloned into distinct DraIII sites of the pME185-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). KhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/clone="IMAGE:1481988"
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/strain="C578L"
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Pred. No. 4.8e-14
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A1529939
799 bp mRNA linear EST 18-MAR-15 ul97c09.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1889392 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HŪMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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/clone lib="Signo mouse liver mlia"
/note="Organ: liver; Vector: pMEL8S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); lst Strand cDNA
was primed with an ollgo(dT) primer
[ATGTGGCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pMEL8S-FL3
vector [5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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lab_host="DH10B"
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strain="C57BL"
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Pred. No. 4.8e-14;
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         AGENCOURT 10789306 NIH MGC_152 Mus musculus cDNA clone IMAGE:6766752 5', mRNA sequence.
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CCA478518.1 GI:24936188
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Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 799)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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EST.
                                                                                                                                                                                                                                                     GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 316
                                                                                                                                                                                                                                                                                                                                                TGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCT 278
                                                                                                                                                                                                                           GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA
                                                                                                                                                                                                                                                                                                                      TGGTCCACTGCCCGCGGAGACACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Clone_lib="Sugano mouse liver mlia"
//Clone_lib="Sugano mouse liver mlia"
//note="Organ: liver; Vector: pwBl8S-FL3; Site_1: DraIII
//note="Organ: liver; Vector: pwBl8S-FL3; lst Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pwBl8S-FL3
vector (5' site CACTGTGG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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/clone="IMAGE:1889392"
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/strain="C57BL"
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Pred. No. 4.8e-14;
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AI790802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Al790802 848 bp mRNA linear EST 02-cuk28b10.71 Sugano mouse kidney mkia Mus musculus CDNA clore IMAGE:1970299 5' similar to gb:x881579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA sequence.
Unpublished (1999)
                                                                                        Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y. Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Sch Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCa
                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 848)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muri
1 (Dases 1 to 811)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house
                                 Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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Tissue Procurement: Bradfield Laboratory
                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI790802.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 136
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/db xref="caxon:10090"
/clone="IMAGE:6766752"
/clone="IMAGE:6766752"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 152"
/clone lib="NIH MGC 152"
/note="Organ: Liver; Vector: pDONR201; Site_1: attP2;
/clone lib="NIH MGC 152"
/note="Organ: Liver; Vector: pDONR201; Site_1: attP2;
/clone lib="NIH MGC 152"
/clone lib="NIH MGC III attP2;
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92.9%;
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Rodentia;
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Pred. No. 4.9e-14;
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                                                                                                          Cardenas, M., McCann, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 811;
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                                                                                                                                       Schurk, R.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 852)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materston, R. and Wilson, R.

Materston, R. and Wilson, R.

Materston, R. and Wilson, R.
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A15283
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AI528304
AI528304.1 GI:4442439
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                    Mus musculus
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//clone lib="Sugano mouse kidney mkia"
//note="Organ: kidney; Vector: pME188S-FL3; Site 1: DraIII
(CACCTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME188-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Site selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers of Tokyo
sequencing: 5' end primer CTTCTGCTCTAAAAGCTTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/db_xref="taxon:10090"
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      TITLE
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                                                       1 (Dases 1 to 605)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu Marra, M., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                     EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ui69d08.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE.1887663 5' similar to 95:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN I PRECURSOR (HUMAN); 9b:X81579 M. musculus mRNA for insulin-like growth factor binding (MOUSE); mRNA
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
Mus musculus
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: custom primer used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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   WashU-HHMI Mouse EST Project
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/note="Torgan: liver; Vector: pMEIBS-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATCTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pMEIBS-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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lab_host="DH10B"
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92.9%;
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Pred. No. 4.9e-14;
D; Mismatches
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6 278

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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 380)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                         Al785039 380 bp mRNA linear EST 02-
ui73a06.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1888018 5' similar to gb:X81579 M. musculus mRNA for
insulin-like growth factor binding (MOUSE);, mRNA sequence.
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                               AI785039
AI785039.1 GI:5332755
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Unpublished (1999)
                                                                                                                                                                                                                                         Mus musculus
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Location/Qualifiers
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Seq primer: custom primer used
                                                                                                                                                                                                                                                           Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGTCCACTGCCCGCGAGACACACACCCAGCGAGCATTGAACACTGCACACGGTCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site 1: DralII (CACCATGTG); lst strand cDNA (CACCATGTG); lst strand cDNA was primed with an oligo (dT) primer
[ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DralII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DralII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTGT). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTGTCTGCTTTAAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="IMAGE:1887663"
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Pred. No. 1.3e-13;
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nes 87; Conserv
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                TCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCC
                                                                                                                                                                                                    TCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCATACGGCCGTCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="Sugano mouse liver mlia"
//clone lib="Sugano mouse liver mlia"
//note="Organ: liver; Vector: pmB:BS-FL3; Site 1: DraIII
/(CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st Strand cDNA
was primed with an oligo(dT) primer
[ATCTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pmE:BS-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). Xhol should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTGTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
                  September
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
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|sex="female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
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                    2005, 06:56:49
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                                                                                                                                                                                                                                                                                               Score 82.2; DB 1;
Pred. No. 8.8e-13;
0; Mismatches 8;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*

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9: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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               US-09-972-916B-4
321
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Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUM
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0 48886	Result No.
321 321 321 219.4 219.4 219 103 76.4	Score
100.0 100.0 68.3 68.3 32.1 23.8	
321 372 270 423 219 423 1500	Length
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US-09-972-916A-4 US-09-972-916A-5 US-09-972-916A-3 US-09-972-916A-6 US-09-972-916A-2 US-09-972-916A-6 US-09-972-916A-6 US-09-972-916A-6	ID
Sequence 4, Appli Sequence 5, Appli Sequence 3, Appli Sequence 6, Appli Sequence 2, Appli Sequence 6, Appli Sequence 1608, Ap	Description

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0-087-192-8	-10-322-281-49	-10-027-632-15	-10-027-632-15	-10-027-632-25	-10-027-632-2556	0-027-632-2	-10-027-632-2556	-10-027-632-25	-10-027-632-2556	-09-980-217-	-10-437-963-79	S-10-437-963-7916	-909-962A-	US-09-909-962A-6	-10-741-600-179	-10-741-601-5	-10-011-585A-7	0-027-632-16	-10-027-632-16433	-10-739-930-546	-09-918-995-22	-10-264-237-82	-10-094-749-9	-10-221-613-14	311-455-	S-10-085-117-17	-09-972-916A-	-09-972-916A-1	S-10-152-319A	-10-388-934-	S-10-893-315-16	US-10-893-315-126	S-10-756-149-14	-09-880-107-2393	S-10-152-319A-	US-10-191-803-73
e 844,	equence 49	equence 15040	e 15	255	255	Sequence 25562,	255	255	25562	1, Ap	O	G.	e 7, App	φ,	equence 17905	equence 5746	equence 76, A	equenc	equence 16433	equence 5461,	equence 22	equence 82	equence 9,	equence 148,	equence 97	e 13		quence 1, Ap	equence 2150	equence 36,	equence 160	e 126,	e 1484	quence 2393,	quence 1613	equence 73,

ALIGNMENTS

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US-09-972-916A-4
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/972,916A CURRENT FILING DATE: 2001-10-10 PRIOR APPLICATION NUMBER: US 60/239,113 PRIOR FILING DATE: 2000-10-11 NUMBER OF SEQ ID NOS: 6 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
                                                                                                                                                   Query Match 100.0%; Score 321; DB 9; Best Local Similarity 100.0%; Pred. No. 9.2e-100; Matches 321; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09972916A Patent No. US20020107198A1
                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 321
  61 GGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTCACAAGCAAAACCAAACT 120
                                                                                    1 TACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCCATGTACACTGGG 60
                                                       1 TACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGG 60
                                                                                                                                                                                                  Length 321;
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Sequence 5, Application US/09972916A

Patent No. US20020107198A1

GENERAL INFORMATION:
APPLICANT: Thule, Peter M.

TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)

CURRENT APPLICATION NUMBER: US/09/972,916A

CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILLING DATE: 2000-10-11

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 5
LEBURTH: 372
TYPE: DNA
ORGANISM: Artificial Sequence
; Sequence
                          RESULT 3
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Best Local
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           3, Application US/09972916A
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                                                                                                                                                                CAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCACCA
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                                                                                   CTTCCGCTACTAGCTAGCCGC 372
                                                                                                                                          CAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 321; DB 9; 100.0%; Pred. No. 9.5e-100;
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APPLICANT: Thule, Peter M.

TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 129/01 (VA)

CURRENT APPLICATION NUMBER: US/09/972,916A

CURRENT FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/239,113

PRIOR FILING DATE: 2000-10-11

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 6

LENGTH: 423
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GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 3
LENGTH: 270
TYPE: DNA
ARCHITECTURE APPLICATION OF INSULING PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                           Matches
                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09972916A Patent No. US20020107198A1
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Best Local Similarity 99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 220;
                                                                                                                                                                                                                                                                                                                 LENGTH: 42
TYPE: DNA
                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                              OTHER INFORMATION: Synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Synthesized
                                                                                                                                                                                           Local Similarity
                                                                                                                                                                         220;
                                    263
                                                                                                                           101 TGTCACAAGCAAAACATATTTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAAT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170
                                                                     230
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221 GTCCACTGCCCGCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGC 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 GTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGC
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                                  TATCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCCACTGCCCGCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGC
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                                                                                                                                                                           Conservative
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                                                                                                                                                                                           Score 219.4;
Pred. No. 7.5
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Pred. No. 6.7e-65;
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                                                                                                                                                                                           .5e-65;
                                                                                                                                                                                                          DB 9;
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RESULT 6
US-09-972-916A-6/c
US-09-972-916A-6/c
; Sequence 6, Application US/09972916A
; Patent No. US20020107198A1
; GENERAL INFORMATION:
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                                                                       ; OTHER INFORMATION: Synthesized US-09-972-916A-6
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US-09-972-916A-2
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US-09-972-916A-2
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TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR PILE REFERENCE: US 1292/01 (VA)

CURRENT APPLICATION NUMBER: US/09/972,916A

CURRENT FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/239,113

PRIOR FILING DATE: 2000-10-11

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 2
LENGTH: 219
TYPE: DNA
ORGANISM: Rattus norvegicus
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Query Match 32.1%; Score 103; DB 9; 1 Best Local Similarity 100.0%; Pred. No. 6.9e-25; Matches 103; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 219; Conservative
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Best Local Similarity
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TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REPERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR PILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                           FEATURE:
                                                                                                                                                             LENGTH: 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCACAAGCAAAACATATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA
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100.0%; Pred. No. 8.7e-65;
tive 0; Mismatches 0;
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                                Length 423;
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 Indels
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Gaps
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US-10-388-934-5

Sequence 5, Application US/10388934
Publication No. US20040005547A1
GENERAL INFORMATION:
APPLICANT: Boess, Franziska
APPLICANT: Suter-Dick, Laura

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CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/22,040
PRIOR FILING DATE: 2000-07-31
PRIOR PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR PILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR PILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-06-19
PRIOR PILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-08-19
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US-09-917-800A-1608
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Best Local
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SEQ ID NO 1608
LENGTH: 1500
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APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
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                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Rattus norvegicus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_013144
                                           299 CACTTCCGCTACTAGCTA 316
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                                                                                                                                                                                                                         l Similarity 77; Conserv
CACTTCCGCTACTATCTA 85
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Pred. No. 1.3e-15;
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                                                                                                                                                                                                                                                                          Length 1500;
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; ORGANISM: Rattus norvegicus (No. US20040005547Alway rat)
US-10-388-934-5
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CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,819
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/305,623
PRIOR FILING DATE: 2001-07-17
PRIOR PPLICATION NUMBER: US 60/369,351
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: US 60/377,611
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 1140
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CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 02005336.9
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 73
LENGTH: 1500
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APPLICANT: PORTER, Mark
APPLICANT: JOHNSON, Kory
APPLICANT: HIGGS, Brandon
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TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
FILE REFERENCE: 44921-5090US
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                                                                                                                                                                                                                OTHER INFORMATION:
                                                                                                                                                                                                                                  ORGANISM: Rattus norvegicus FEATURE:
                                                                                                                                                                                                                                                                       TYPE: DNA
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CACTTCCGCTACTAGCTA 316
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98.7%;
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Pred. No. 1.3e-15;
0; Mismatches 1;
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Pred. No. 1.
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US-09-880-107-2393
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US-10-152-319A-1613
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; LENGTH: 1500
; TYPE: DNA
                                                      Sequence 2393, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
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Publication No. US20040072160A1
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APPLICANT:
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                  APPLICANT: Gene Logic, Inc. TITLE OF INVENTION: Gene Expression
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PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,807
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PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-06-13
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FILE REFERENCE: 44921-5028-WO
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PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR FILING DATE: 2001-11-01
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PRIOR APPLICATION NUMBER: US 60/303,808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Rattus norvegicus
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TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER FILE REFERENCE: file CURRENT APPLICATION NUMBER: US/10/756,149

CURRENT FILING DATE: 2004-01-12

NUMBER OF SEQ ID NOS: 5818

SOFTWARE: Patentin version 3.2

SEQ ID NO 1484
LENGTH: 6128

TYPE: DNA

ORGANISM ...
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CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOPTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2393
LENGTH: 6128
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US-10-756-149-1484
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US-10-756-149-1484
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                                     ACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCC------GTGCTGCCG 178
                                                                                             CCACTTC 304
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                                                                     TCCTCCCACCAGCGGTTTGCGTAGGGCCTTGGGTGCACTAGCAAAACTTATTTTGA
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               ACACTCAGCTCCTAGCGTGCGGCGCTGCCAATCATTAACCTCCTGGTGCAAGTGGCGCGG
                                                                                                                                Conservative
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Pred. No. 3.8e-11;
0; Mismatches 72;
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Pred. No. 3
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       US-10-893-315-160

Sequence 160, Application US/10893315

Publication No. US20050147987A1

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH TYPE II DIABETES A

TITLE OF INVENTION: USES THEREOF

FILLE REFERENCE: CL000786

CURRENT APPLICATION UNMBER: US/10/893,315

CURRENT FILING DATE: 2004-07-19

BELTOR ARPLICATION
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US-10-893-315-126
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PRIOR APPLICATION NUMBER: 60/231,397
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Sequence 126, Application US/10893315

| Publication No. US20050147987A1 |
| GENERAL INFORMATION: US20050147987A1 |
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS |
| TITLE OF INVENTION: USES THEREOF |
| TURNER OF ILLING DATE: 2004-07-19 |
| PRIOR APPLICATION NUMBER: 60/231,397 |
| PRIOR APPLICATION NUMBER: 5000-09-08 |
| NUMBER OF SEQ ID NOS: 2172 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO: 126 |
| LENGTH: 9113 |
| TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.9%;
Best Local Similarity 63.2%;
Matches 156; Conservative
2074 CCGCTCC 2080
                                                          CCACTTC 304
                                                                                                                    ----CATCCAGCGAGCATCTGCCGCCGCGCGCCGCCACCCTCCCAGAGAGCACTGGCCA
                                                                                                                                                                     CACAAACCCAGCGAGCATTGAACACTGC-ACACGGCCATCTGCCCAGAGAGAGCTGTGACCA
                                                                                                                                                                                                                                            CCTGTGCCCTTTATAAGGTGCGCGCCTGTGTCCAGCGAGCATCGGCCACCGCCATCC----
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Pred. No. 4.3e-11;
0; Mismatches 72;
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IN KNOWN GENES ASSOCIATED DIABETES AND OBESITY, METHODS OF DETECTION AND

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CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 02005336.9
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
SOFTWARE: Patentin version 3.1
SEQ ID NO 36
LENGTH: 13011
TYPE: DNA
ORGANISM: Rattus norvegicus (No. US20040005547Alway rat)
US-10-388-934-36
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US-10-388-934-36/c
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Publication No. US20040005547A1
GENERAL INFORMATION:
APPLICANT: Boess, Franziska
APPLICANT: Suter-Dick, Laura
APPLICANT: Wolf, Detlef
TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
                                                                                                                                                        Query Match
Best Local Similarity
Matches 60; Conserv
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                                   CGCCCATG 102
                                                                                            TGCCCCGTGCGCCATGTACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTG 94
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                                                                                                                                                  17.2%; Score 55.2; DB 17; Length 13011; ilarity 88.2%; Pred. No. 4.2e-08; Conservative 0; Mismatches 8; Indels 0;
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Search completed: September Job time: 944.893 secs

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Title:
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Maximum Match 100%
Listing first 45 summaries
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Match Length
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Gapop 10.0 , Gapext 1.0
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    Copyright
    GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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US-09-949-001-30
US-09-949-001-36
US-08-945-140-11
US-08-949-016-11786
US-09-949-016-1205
US-09-949-016-12194
US-09-949-016-13194
US-09-949-016-11816
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US-09-949-016-13895
US-09-949-016-13895
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US-09-9270-767-13109
US-09-909-962A-7
US-09-909-962A-7
US-09-909-56A-7
US-09-909-56A-7
US-09-909-56A-7
US-09-909-56A-177
US-09-902-540-1177
US-09-902-540-11745
US-09-949-016-11745
US-09-949-016-11745
US-09-949-016-11745
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US-09-949-016-11745
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Sequence 30, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 17205, Appl Sequence 17205, App Sequence 138, App Sequence 2153, Appl Sequence 2153, Appl Sequence 13895, A Sequence 13895, A Sequence 13895, A Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 15639, A Sequence 15639, A Sequence 3, Appl Sequence 3659, A Sequence 1177, App Sequence 1177, App Sequence 1177, App Sequence 11745, A Sequence 11745, A Sequence 11745, A Sequence 10411, App Sequence 11990, App Sequence 10411, App Sequence 10411, App Sequence 11990, App Sequence 119
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RESULT 2
US-09-949-001-36
; Sequence 36, Application US/09949001
; Patent No. 6825336

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CACA	AGC	ACAC		i m	1.6 9.1.1.2 9.1.3.1 9.3.3.1 9.
CATC	AGCC	GGGG CTCAC	AGGA,	19.98 Similarity 63.28 6; Conservative	11.6 9.8 9 11.2 9.7 11.2 9.7 31 9.7 31 9.7 0.6 9.5 2 0.6 9.5 2 9.8 9.3 9.8 9.3 9.8 9.3 9.6 9.2 1 9.6 9.2 1 9.6 9.2 1 9.6 9.2 2 9.6 9.2 1 9.6 9.2 2 9.6 9.2 1 1.0 CENTER, J. INVENTION: PERENCE: CLOOO PATE: CLOOO
CAG		ATC	\$:y ervat	
GAG	TATA	TAG	36-69 	19.9 63.7 ive	99749 4 US- 601 4 US- 601 4 US- 1888 4 US- 1887 4 US- 897 4 US- 28493 4 US- 1011 4 US- 1027 4 US- 1620 4 US- 1620 4 US- 22404 4 US- 22404 4 US- 22404 4 US- 22407 4 US- 22407 1 US- 22407 1 US- 22408 1 US- 22408 1 US- 22408 1 US- 22409
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CACAAACCCAGCGAGCATTGAACACTGC-ACACGGCCATCTGCCCAGAGAGCTGTGACCA 	AGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGA	ACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCGTGCTGCCG 	TCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTCACAAGCAAAACAAAC	Score Pred. 0; Mi	
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6	CAGC		ATGI	DB .3e-	949-016-16518 949-016-16969 949-016-1341 949-016-1341 949-016-1741 949-016-17983-12 067-782A-1 489-039A-2808 949-016-117389 949-016-11859 949-016-11859 949-016-11859 949-016-15398 GNMENTS IS, METHODS O 9,001
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 9174
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL000789
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Best Local Similarity
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CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/231,323
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CHEN, Ruihuan
APPLICANT: DOIRON, Bruno
APPLICANT: KAHN, Axel
TITLE OF INVENTION: GLUCOSE-INDUCIBLE RECOMBINANT VIRAL
TITLE OF INVENTION: VECTOR
NUMBER OF SEQUENCES: 10
                           FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: FR 95/04558
APPLICATION NUMBER: FR 95/04558
                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,140
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                   FILING DATE:
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APPLICATION DATA:
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500 Arcola Road, Mailstop 3C43
                                                                                                                                                                                                                                                                    USA
                   14-APR-1995
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RESULT 4
US-08-791-849A-14/c
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Patent No. 5914449
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                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/791
FILING DATE: January 30, 1997
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APPLICANT: Makoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (610) 454-3808 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, J
REGISTRATION NUMBER: 33,
                                                                                                                           REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                         CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
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LENGTH: 194 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Makoto MURASE et al.
TITLE OF INVENTION: Method for Increasing Storage
TITLE OF INVENTION: Lipid Content in Plant Seed
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 12-APR-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A. ZIP: 20005
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REFERENCE/DOCKET NUMBER: EX950
            STRANDEDNESS:
                                                                                                             TELEFAX:
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                                            LENGTH:
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Local Similarity 88.2%;
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        H: 13011 base pairs nucleic acid DEDNESS: double
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805 Fifteenth Street, N.W., #700
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linear
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Pred. No. 1.6e-08;
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RESULT 6
US-09-949-016-17205/c
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US-09-949-016-11786/c
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Best Local S
Matches 60
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Best Local S
Matches 48
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SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 11786
LENGTH: 15108
TYPE: DNA
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11786, Application US/09949016
Patent No. 6812339
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NAME/KEY:
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LOCATION:
LOCATION:
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Local Similarity 88.2%;
les 60; Conservative
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                                                                                                                                                                                                                Conservative
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6152..6283, 6418..6604, 6921..7191, 7302..7452, 7665..7817, 7911..8077
9298..9479, 10163..10269)
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78.7%;
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Pred. No. 0.011;
0; Mismatches 13; Indels 0;
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Pred. No. 1.1e-07;
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US-09-949-016-17205
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APPLICANT: Wolkmuth, Wayne
APPLICANT: Wolkmuth, Wayne
APPLICANT: Wolker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
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; SEQ ID NO 138
; LENGTH: 3054
; TYPE: DNA
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
RIOR FILING DATE: 2000-09-08
RUMBER OF SEQ ID NOS: 207012
                                                                                                                                                    Query Match
Best Local Similarity
Matches 57; Conserv
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LENGTH: 15108
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                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6426186 336987.1CB1
                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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                                    GCCAGAGTCCAGGAACCACGGGAGTGCCCCG 92
                                                                         ACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGGG
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78.7%;
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Pred. No. 0.011;
0; Mismatches 13;
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GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19194
                                                                                      Best Local Similarity 55.3 Matches 68; Conservative
                                                                                                                                Query Match
                                                                                                                                                                                                                                                         SEQ ID NO 73784
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                                                                                                                                                                                                                                                                                                                  APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                                                                     LENGTH: 601
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                            181 CCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACA 240
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Pred. No. 0.14;
0; Mismatches
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Pred. No. 0.14;
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US-09-949-016-2153/c
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             APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT PAPLICATION NUMBER: 00/29/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                      Sequence 74, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows
SEQ ID NO 2153
LENGTH: 2393
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
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LENGTH: 2408
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Pred. No. 0.26;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 5007-09-08
INUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASCSEQ for Windows Version 4.0
SEQ ID NO 11816
LENGTH: 7561
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US-09-949-016-13895/c
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US-09-949-016-11816/c
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; ORGANISM: Human
US-09-949-016-74
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
                                                                                                                      Sequence 13895, Application US/09949016 Patent No. 6812339
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Best Local Similarity
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ORGANISM: Human
-09-949-016-11816
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Best Local Similarity
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Pred. No.
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Pred. No. 0.
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Sequence 29006, Application US/09270767
Patent NO. 6703491
GENERAL INFORMATION:
APPLICANT: Hemburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29006
LENGTH: 364
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; ORGANISM: Drosophila melanogaster
US-09-270-767-29006
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US-09-270-767-29006
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; ORGANISM: Human
US-09-949-016-13895
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PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                    Query Match 10.4%; Score 33.4; DB 4; Best Local Similarity 51.2%; Pred. No. 0.38; Matches 105; Conservative 0; Mismatches 96;
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LENGTH: 7562
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Best Local Similarity
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340
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                                 258 GAĄCĄCTGCACACGGCCATCTGCCC 282
                                                                                                                                                      220 GCCGAACAGGACTTCGTGGCCATGCTCACCGCCTGGTACATGTCCCGGCTATTATACGGGC
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 GCAPACAGCCATCAGCCACCAGTCC
                                                                           CCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACAAACCCAGCGAGCATT 257
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RESULT 15 US-09-270-767-13109

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; Sequence 13109, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 67517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13109
; ENGTH: 761
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13109
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Search completed: September 1, Job time: 102.545 secs
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                      Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
214.4
1181.8
1188.8
198.2
79.2
76.4
76.4
76.4
76.4
76.4
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63.8
63.8
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         August 31, 2005, 13:10:38 ; Search time 2316.24 Seconds (without alignments) 7782.159 Million cell update
                                                                                                                                                                                         Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4708233 seqs, 24227607955 residues
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372
GenEmbl: *
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gbon: *
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10
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AL607124
BC013345
AY560836
AX401932
AX401932
AX827271
O RATIGFB
AX163782
                                            RATIGFBA
BC078889
AY095345
AX409747
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AC136382
HUMIGFBP1
AY434089
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                             HUMIGFBP1A
G19994
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Compugen Ltd.
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                        M84484 Rattus norv
AC136382 Rattus no
X67493 M. musculus
AL607124 Mouse DNA
BC013345 Mus muscul
AY560836 Spermophi
AX401932 Sequence
M58634 Rat IGF bin
AX163782 Sequence
L22999 Rat insuli
BC078889 Rattus no
AX1637845 Papio anu
AX409747 Sequence
M74587 Human insuli
G19994 sWSS752 Eri
       M59316 Human insul
AY434089 Homo sapi
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41	41.4	42.4	42.4	42.6	42.6	42.6	44.2	44.2	44.4	44.6	44.6	44.6	47.4	47.4	52	54.4	55.2	55.2	55.2	55.2	55.2	60.8	62.2	62.2	62.2
11.0 81704	11.1 200340	11.4 187397	11.4 170654	11.5 186314	11.5 53370	11.5 43295	11.9 215533	11.9 206515	11.9 1480	12.0 259329		12.0 184889	12.7 231241			6	13	14.8 13011	14.8 13011	14.8 194		16.3 448	16.7 200935	16.7 189932	16.7 141539
9 AC110299	9 AC100797	2 AC114566	10 AC116502	10 AC003694	9 AL592071	2 AC006177	2 AC149086	10 AC140332	10 RATIGFBP1	2 AC109570	2 AC097952	9 AL442125	2 AC097039			9 HUMIGFBPB1	10 RNLPKG	6 AX827302	6 E14395	6 AR175909	6 A57715	11 G67139	2 AC148834	2 AC146117	9 AC146152
AC110299 Homo sapi	AC100797 Homo sapi	AC114566 Mus muscu	AC116502 Mus muscu	AC003694 Mus muscu	AL592071 Human DNA	AC006177 Homo sapi	AC149086 Mus muscu	AC140332 Mus muscu	M89791 Rattus norv	AC109570 Rattus no	AC097952 Rattus no	AL442125 Human DNA	AC097039 Rattus no	M17088 Rat pyruvat	G67173 IGFBP1 5'A	M23592 Human insul	X05684 Rat L-PK ge	AX827302 Sequence	E14395 gDNA encodi	AR175909 Sequence	A57715 Sequence 1	G67139 IGFBP1 X1.1	AC148834 Pan trogl	AC146117 Pan trogl	AC146152 Pan trogl

ALIGNMENTS

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LOCUS
DEFINITION
ACCESSION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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COMMENT
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RATILGEZ
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Best Local Similarity
Matches 218; Conserva
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                                                                                                               813
                   264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insulin-like growth factor.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M84484.1 GI:204927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RATILGEZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus.
CCAGCATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGG
                                                                                                                              TGCGCCCATGTCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCC
                                                                             CTGACAATCATTAACCCGTGCTGCCGAGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAG
                                                                                                            TGTGCGGAGCTCACAAGCAAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCC
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                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                               /tissue_type="liver"
/dev_stage="adult"
                                                                                                                                                                                                                                                                               /db_xref="taxon:10116"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                              mol_type="genomic DNA"
strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                              . .1181
                                                                                                                                                                                                                                                                                                                                              organism="Rattus norvegicus"
                                                                                                                                                                    57.6%; Score 214.4; DB 10; 97.3%; Pred. No. 1.5e-51; tive 0; Mismatches 6;
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JOURNAL
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                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                              Biswald, K., Blair, J., Balakenbug, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, E., Chu, J.,
Cleveland, C., Cockreil, R., Cac, Coyle, M., Cree, A., D'Sozaa, L.,
Delgado, O., Denson, S., Denamo, C., Ding, Y., Dinh, H., Divya, K.,
Delgado, O., Denson, S., Denn, A., Durbin, K., Daval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, M., Forbes, L., Foster, M., Fascer, M., Gabres, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawe, A., Henderson, M., Hernandez, J.,
Hernandez, R., Hines, S., Hladin, S. L., Hodgson, A., Hoptes, M.,
Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawe, A., Henderson, M., Hernandez, J.,
Hernandez, R., Hines, S., Hladin, S. L., Hodgson, A., Hoptes, M.,
Gunaratne, P., Haelland, W., Hamil, C., Hamilton, C., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Johnson, A.,
Jockson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Johnson, A.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Kraft, C.L., Lebow, H., Lozado, R. J., Liu, J.,
Liu, J., Liu, W., London, P., Longacre, S., Lopez, J.,
Liu, J., Liu, W., London, P., Longacre, S., Lopez, J.,
Liu, J., Liu, W., Martin, K., Martin, R., Martinez, E.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhiney, S., Melled, M., Murphy, M., Nairi, N., Morgan, M., Morris, K.,
Morris, S., Mundaea, M., Murphy, M., Nairi, L., Nankervis, C., Neal, D.,
Primus, E., Pull, L., Puazo, M., Quiroz, J., Rachlin, E.,
Perez, A., Perez, L., Pfannkoch, C., Potoper, F., Poindexter, A.,
Song, X., Taelos, Z., Usani, K., Marti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                933
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Rat Genome Sequencing Consortium
                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC136382.1 GI:24462257
HTG; HTGS_PHASE1.
Rattus norvegicus (Norway rat)
                                     Unpublished
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                     (bases 1 to 185148)
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Submitted (01-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.h
NOTE: This is a 'working draft' sequence. It currently
consists of 63 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of rechemistry: Dye-terminator Big Dye: 100% of rechembly program: Phrap; version 0.990329 Consensus quality: 135613 bases at least Q40 Consensus quality: 140849 bases at least Q30 Consensus quality: 145680 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center clone name: CH230-97018
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33994:
35373:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (23-JUL-1992) R.A. Taub, Univ. of Pennsylvania, Howard Hughes Medical Institute, Clinical Research Bldg., Room 475, 422 Curie Boulevard, Philadelphia, PA 19104-6145, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 1363)
Mohn,K.L., Waddle,J.R. and Taub,R.
Comparison of mouse and human IGFBP-1 genes reveals a potential
insulin-responsive sequence and conservation of all intron/exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1363)
Lee,J., Greenbaum,L., Haber,B.A., Nagle,D., Lee,V., Miles,V., Mohn,K.L., Bucan,M. and Taub,R.
Structure and localization of the IGFBP-1 gene and its expression during liver regeneration
Hepatology 19 (3), 656-665 (1994)
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/cell_type="fibroblast"
/clone_lib="genomic, lamb
/dev stage="embryo"
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/codon_start=1
/product="insulin-like growth factor
/protein_id="CAA47832.1"
/db_xref="GOA: P47876"
/db_xref="GOA: P47876"
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                                                                                                                                                                                                                       sequences"
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/mol_type="genomic DNA"
/strain="NIH Swiss"
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                                                                                                                                                                                                                                                                                                                                                                                                                              clone="JW2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:10090"
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for insulin-like
                                                                                                                               cap
                                                                                                                                                                                                                                                                                                                 consensus
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                                                                                                                                 Bite"
                                                                                                                                                                                                                                                                                                                                                                      lambda FIX II"
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                                                                          factor binding protein-1"
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846 323 786 263

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RESULT 4
AL607124
      FEATURES
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ORGANISM
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TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (11-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBLO 15A, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Con Apr 12, 2002 this sequence version replaced gi:19847866. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations cogether with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences wit only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                              regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; TT:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                       http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-20C9 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                              database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oliver, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL607124.15
HTG.
                                 VECTOR: pBACe3.6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse DNA sequence from clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTGTAGAGCTCACAAGCAAAACAAACTTATTTTGAACACTGGGGTCCTAGCACGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCGCCCATGTCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGCATGGTCCACTGCCCGCGGAGACACACACCCAGCGAGCATTGAACACTGCACACGG
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PVPASCPEISRPAGCGCCPTCALPMGAACGVATARCAQGLSCRALPGEPRPLHALTRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGASLPEPAAPATSTLFSSQHE"
Location/Qualifiers
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Pred. No. 4.3e-44;
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ROD 11-APR-2002

11, complete

source

/organism="Mus musculus
/mol_type="genomic DNA"
/db_xref="taxon:10090"

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REFERENCE
AUTHORS
TITLE
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BC013345
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                                                                                                                                     REMARK
                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
RS Klausher, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buettw, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schect, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
MCKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakeeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2539
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                   NIH-MGC Project URL: http://mgc.
Contact: MGC help desk
                                                                                                                                                                               Direct Submission
Submitted (31-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC013345 Inear ROD Mus musculus insulin-like growth factor binding protein (CDNA clone MGC:14075 IMAGE:4161889), complete cds.
                                                                                                                                                                                                                                                                                                 Strausberg, R
                                                                                                                                                                                                                                                                                                                                                                                human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTGTAGAGCTCACAAGCAAAACCTAATTTTGAACACTGGGGTCCTAGCACGCTGCC
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Pred. No. 5.5e-44;
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sequences with

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Best Local Similarity
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Li,Y., Klimanis,D. and Hallenbeck,J.M.
Cloning and characterization of insulin-like growth factor binding protein 1 (IGFBP-1) from thirteen-lined ground squirrel
                                                                                                                                                                                                                                                                                                                                 Spermophilus tridecemlineatus protein 1 (IGFBP1) mRNA, comp AY560836
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Series: IRAK Plate: 18 Row: i Column: 20
This clone was selected for file the sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Similarity but not identity to protein.
                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                  Spermophilus tridecemlineatus (thirteen-lined ground squirrel) Spermophilus tridecemlineatus
                                                                                                                                                                                                                                                                                                         AY560836.1 GI:45505308
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Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                           AY560836
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                                                                                                                                 Spermophilus.
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                                                                                                (bases 1 to 1507)
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/product="insulin-like growth factor binding protein 1"
/protein_id="AAH13345_1"
/db_xref="Gi:15426483"
/db_xref="MGI:96436"
/db_xref="MGI:964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNKNGFYHSKQCETSLDGEAGLCWCVYPWSGKKIPGSLETRGDPNCHQYFNVHN"
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/db_xref="LocusID:16006"
/db_xref="MGI:96436"
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/tissue type="Liver, normal. 5 mc/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B"
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/mol_type="mRNA"
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Pred. No. 1.2e-17;
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AX401932
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Sequence 1608 from Patent WO0210453
AX401932
                                                                                                                                                                                             Mendrick, D.,
Elashoff, M.R.
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Direct Submission
                                                                                                                                                                         Molecular toxicology
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                                                                                                                               Logic,
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                                                                                                                                                   WO 0210453-A
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/mol_type="unassigned DNA"
/mb.type="unassigned DNA"
/db xref="taxon:10116"
/note="EMBL/GenBank Accession No. NM_013144"
                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="insulin-like growth factor
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/db_xref="GI:45505309"
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/mol_type="mRNA"
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Rodentia;
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1608 07-FEB-2002;
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                                                                                                                                              Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Rodentia;
                                                                     1 (bases 1 to 1500)

Mohn, K.L., Melby, A.E., Tewari, D.S., Laz, T.M. and Taub, R. The gene encoding rat insulinlike growth factor-binding is rapidly and highly induced in regenerating liver Mol. Cell. Biol. 11 (3), 1393-1401 (1991)
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IGF binding protein-1.
Rattus norvegicus (Norway rat)
                                     Original
                                                                 91141487
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Sequence 5 from Patent EP1344834.
AX827271 GI:39837360
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Mammalia; Eutheria;
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source text: Rat, cDNA to mRNJ
Location/Qualifiers
1. .1500
/organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
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98.7%;
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Rodentia;
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Pred. No. 2.6e-1
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Sciurognathi; Muridae;
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61
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AX163782
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                 Patent: WO 0138579-A 46 31-MAY-2001;
Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                           Gould-Rothberg, B.E., Dipippo, V.A., Ramseh, T.M. and Gerwein, R.W. Method of identifying toxic agents using nsaid-induced differential
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CACTTCCGCTACTATCTA
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                                                                          CACTTCCGCTACTAGCTA 367
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235. .975
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                                                                                                                                                                                       /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="Fisher"
/db_xref="taxon:10116"
/tissue_type="regenerating liver"
/dev_stage="adult"
160 _ 978
                                                                                                                                                                                                                                                   Location/Qualifiers
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/product="IGF binding
/protein_id="AAA41380
/db_xref="GI:204733"
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                                                                                                                                Score 76.4;
Pred. No. 2.
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Pred. No. 2.6e-11;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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insulin-like growth factor binding
Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RATIGFBA
Rat insulin-like
                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus
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                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="insulin-like growth factor binding protein"
/protein id="AAA82581.1"
/db xref="G::1099473"
/db xref="G::1099473"
/db xref="G::1099473"
/db xref="G::009473"
/fdb xref=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNKNGFYHSKQCETSLDGEAGLCWCVYPWSGKKIPGSLETRGDPNCHQYPNVQN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="IGFBP-1"
join(153. .525,1850.
/gene="IGFBP-1"
                                                                                                                                                                                                                                                                                                                                3003. .4089
/gene="IGFBP-1"
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                                                                                                                                                                                                                                                                                                    number=3
                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="IGFBP-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="liver"
/dev_stage="adult"
/tissue_lib="Clontech EMBL-3 SP6/T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Rattus norvegicus"
|mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                     number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Sprague-Dawley"
/db_xref="taxon:10116"
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                                                                                                             20.5%;
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                                                                                 Score 76.4; DB 10;
Pred. No. 2.8e-11;
0; Mismatches 1;
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                                                                                                                                                                through the I.M.A.G.E. Consortium/LINL at: http://image.linl.gov
Series: IRAK Plate: 184 Row: e Column: 23
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6981079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Express Genomics cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) cDNA Sequencing by: Sequencing Group at the Stanford Human Genome DNA Sequencing by: Sequencing Group at the Stanford, CA 941 Center, Stanford University School of Medicine, Stanford, CA 941 Web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bass 1 to 1510)
Director MGC Project.
Direct Submission
Submitted (02-AUG-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/mol_type="mRNA"
/db_xref="taxon:10116"
                                                                                  organism="Rattus norvegicus"
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                                                                                                                                                                                                      Direct Submission
Submitted (11-APR-2002) Department of Obstetrics and Gynecology, Submitted (11-Illinois at Chicago, 820 S. Wood, Chicago, IL 60612,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Papio anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 3886)
Kim, J.J., Jaffe, R.C. and Fazleabas, A.T.
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                                                   /organism="Papio anubis"
/mol_type="genomic DNA"
/db_xref="taxon:9555"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MPBFLTVVSWPFLILLSFQVRVVAGAPQPWHCAPCTAERLELCP PVPASCPEISRPAGCGCCPTCALPLGAAAGGVATARCAGGLSCRALBGEBRPLHALTRG GGACVLEPAAPATSSLSGSQHEEAKAAVASEDELAESPEMTEBGLLDSFHEMAPSFB GGACVLEPAAPATSSLSGSQHEEAKAAVASEDELAESPEMTEBGLLDSFHEMAPSFB GGAGVLEPAAPATSSLSGSQHEEAKAAVASEDELAESPEMTEBGLLDSFHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPATSCHAPAT
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/protein_id="AAH78889.1"
/db_xref="GI:50927647"
/gene="IGFBP-1"
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/db_xref="RATMAP:44422"
/db_xref="RGD:2872"
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/db_xref="LocusID:25685"
/db_xref="RATMAP:44422"
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/clone_lib="NIH_MGC_236"
/lab_host="DH10B"
/note="Yector: pExpress1"
                                                                                                                                                                              ocation/Qualifiers
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Pred. No. 4.3e-08;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                  Alvares,C., Horne,D., Peres-da-Silva,S.;
Gene expression profiles in liver cancer
Patent: WO 0229103-A 2394 11-APR-2002;
GENE LOGIC INC (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2394 from Patent WO0229103. AX409747
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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ACACTCAGCTCCTAGCGTGCGGCGCTGCCAATCATTAACCTCCTGGTGCAAGTGGCGCGG
                   ACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCC------
                                                              CACTTC 355
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3655. .>3886
/gene="IGFBP-1"
/codon start=1
/product="insulin-like growth factor binding protein-1"
/protein_id="AAM3273.1"
/db_xref="G1:2083765"
/translation="MSEVPVARVWIVILLLITVQVGVTASAPWQCAPCSAEKLALCPPV
PASCSEVTRSAGCGCCPMCALPLGAACGVATAR"
                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                         note="EMBL/GenBank Accession No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="IGFBP-1"
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63.2%;
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                                                                                                                                       Score 63.8; DB 6;
Pred. No. 1.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Original source text: Homo sapiens Charon4A) liver DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contiguous localization of the genes encoding human insulin-like growth factor binding proteins 1 (IGBP1) and 3 (IGBP3) on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M74587.1 GI:184811
insulin-like growth factor binding protein Homo sapiens (human)
Homo sapiens
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tissue_lib="lambda Charon4A"
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                                                                                               CCTGTGCCCTTTATAAGGTGCGCGCTGTGTCCAGCGAGCATCGGCCACCGCCATCC----
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ALIGNMENTS

REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 1 BF236974 LOCUS ORIGIN FEATURES COMMENT DEFINITION Query Match Best Local Sim Matches 103; TITLE JOURNAL source Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAM9443 row: j column: 02
High quality sequence stop: 581.
Location/Qualifiers Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1013)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D. BF236974 1013 602026605F1 NCI_CGAP_Li9 Mus Mus musculus BF236974.1 GI:11150891 Mus musculus (house mouse) mRNA sequence. Similarity Conservative /lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Li9"
/note="Organ: Ilver; Vector: pCMV-SPORT6; Site_1: Not Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library." organism="Mus musculus" /mol_type="mRNA" /strain="FVB/N" db_xref="taxon:10090" clone="IMAGE:4161889" .1013 26.4%; 92.8%; <u>,</u> Score 98.2; DB 2; Pred. No. 5.9e-17; 0; Mismatches 8; bp mRNA linear EST 14-NOV-2000 musculus cDNA clone IMAGE:4161889 5', 8; Length 1013; Murinae; Mus.

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257 TGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTG 316

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Genome Exploration Research Group, RIKEN Genom Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045,
Tel: 81-45-503-9222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY783538 RIKEN full-length enriched, 17.5 days embryo Mus musculus cDNA clone L930176D05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 310)
                                                                                                                                                           Similarity 92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yoshihide Hayashizaki
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TGCCCAGAGAGCTGTGACCACCACTTCCGCTACCTAGCTA 367
                                                                     ATGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTC
                                                                                             ATGGTCCACTGCCCGCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                               /tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5
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/clone="L930176D05"
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Pred. No. 4.2e-14;
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RESULT 4
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Division of Experimental Animal Research in Riken contributed to
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The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
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                                                                                                                                                                                                                                                                                  ATGGTCCACTGCCCGCGGAGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTC
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/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
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/strain="C57BL/6J"
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                     269 ATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATC
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Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia
Genome Res. 13 (6B), 1273-1289 (2003)
                 A1785918 401 bp mRNA linear EST 02-
ui78h05.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1888569 5' similar to gb:X81579 M.musculus mRNA for
insulin-like growth factor binding (MOUSE); mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY771317
354 bp mRNA linear EST 23-MAR-2/BY771317 RIKEN full-length enriched, 17.5 days embryo whole body musculus cDNA clone L930052015 5', mRNA sequence.
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Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
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Pred. No. 4.3e-14;
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ABO bp mRNA LINEAL LOCALITY OF THE AUTOLOGY OF THE A
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Other_ESTs: ui78h05.x1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
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The WashU-NCI Mouse EST Project 1999
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 401)
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Fax: 314 286 1810
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Location/Qualifiers
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/note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
(CACCATGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI shoul
be used to isolate the cDNA insert. Size selection was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' primer CGACCTGCAGCTCGAGCACA."
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/strain="C57BL"
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/mol_type="mRNA"
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/lab_host="DH10B"
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Pred. No. 8.5e-14;
D; Mismatches 7;
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AI530146
706 bp mRNA linear EST 18-MAR-19 u189f09.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1889609 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HŪNAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 480)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                           \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashU-HIMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
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AI196314.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                     TGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCT
                                                                                                                                                                                                                                                                                    GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 367
                                                                                                                                                                                                                                                                                                                                        TGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Clone_lib="Sugano mouse liver mlia"
//Clone="Organ: liver; Vector: pWELBS-FL3; Site 1: DraIII
//CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pMELBS-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTGTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strain="C57BL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 86.8; DB 1;
Pred. No. 8.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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RESULT 8
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ACCESSION
                                                                                                                                   DEFINITION
                                                                                                                                                                                  FOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 TGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCT 329
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AI530146
AI530146.1
                                     A1098594 Tinear EST 20-
ue31e07.yl Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1481988 5' similar to gb:X81579 M.musculus mRNA for
insulin-like growth factor binding (MOUSE); mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91;
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The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                         GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGTCCACTGCCCGCGAGACACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Sugano mouse liver mlia"
//clone_lib="Sugano mouse liver mlia"
//note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTGT); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATCTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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/strain="C57BL"
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sex="female"
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Pred. No. 9.5e-14;
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RESULT 9
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AUTHORS
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                                                                                  DEFINITION
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Best Local :
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                                                                                                                                                                                                                                                                     330
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AI530313
AI530313
AI530313
AI530313
AI59101.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1889785 5' similar to gb:M59315 rnal INSULIN-LIKE GROWTH
FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus
mRNA for insulin-like growth factor binding (MOUSE);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 314 400 to the Benail: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1996)
Contact: Marra M.Mouse EST Project
WashU-HMM Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 765)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuo,Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:930344
Seq primer: custom primer used
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                        GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 367
                                                                                                                                                                                                                                                                                                                                                            TGGTCCACTGCCCGCCGAGACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCT
                                                                                                                                                                                                                    GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 98
                                                                                                                                                                                                                                                                                                              TGGTCCACTGCCCGCGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence stop: 395.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pWE185-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACATGTG); 1st Strand cDNA was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME185-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI shoul be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library
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/db_xref="taxon:10090"
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92.9%;
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Pred. No. 9.7e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 270
                                                                                                                                                                                                                                                                                           330 GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 367
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AIS29939

799 bp mRNA linear EST 18-MAR-1: ui87C09.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1889392 5' similar to gb:m59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
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AI530313.1
EST.
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The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 785)
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Location/Qualifiers
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/note="Organ: liver; Vector: pME18S:FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACARGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S:FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). Xhou shoul
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' primer CGACCTGCAGCTCGAGCACA."
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/strain="C57BL"
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/lab_host="DH10B"
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92.9%;
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Pred. No. 9.7e-14;
D; Mismatches 7;
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; Murinae; Mus
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Seq primer:
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The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
                     CA478518
CA478518.1 GI:24936188
                                                              AGENCOURT 10789306 NIH MGC 152 Mus IMAGE:6766752 5', mRNA sequence.
                                                                                                               CA478518
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Location/Qualifiers
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//clone_lib="Sugano mouse liver mlia"
//note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACCATGTG); lst strand cDNA
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[ATCTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
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and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTGG), XhoI should
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Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTGTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/mol_type="mRNA"
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/lab_host="DH10B"
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/clone="IMAGE:1889392"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 86.8; DB 1;
Pred. No. 9.8e-14;
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                              AUTHORS
                                                                                                                                                                                                                 ORGANISM
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  JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 TGGTCCACTGCCCGCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCT 329
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               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae 1 (bases 1 to 848)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,? Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurktter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCanu Waterston,R. and Wilson,R.

WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                AI790802

848 bp mRNA linear EST 02-cuk28b10.yl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1970299 5' similar to gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; I
1 (bases 1 to 811)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Unpublished (1999)
                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov platee: LLKM00138 row: m column: 23 High quality sequence.stop: 536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Bradfield Laboratory
                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                 AI790802.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Mark Bittinger
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:6766752"
/lab host="DH10B (phage-resistant)"
/clone lib="NHH MGC 152"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                               GI:5338518
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                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                Cardenas, M., McCann, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 811;
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                                                                                                                            Beck, C., Wylie, T.,
                                                                                                                                                                                                                                                                                                                                                                                          EST 02-JUL-1999
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                                                                                  Schurk, R.,
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ACCESSION
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                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
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Best Local S
Matches 91
        TITLE
                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 852)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                      AIS28304

AIS28304

BS2 bp mRNA linear EST 18-MAR-1: ui95g10.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1890210 5' similar to gb:M59316 rna1 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    μ.
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                                                                                                                                                                                                                                                      EST.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                AI528304
AI528304.1
                                                                                                                                                                                                                                                                                                                                                                   sequence.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGI:987039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 98
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n quality sequence stop: 514.
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Location/Qualifiers
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//Clone_Torgan: kidney; Vector: pME18S:FL3; Site 1: DraIII
(CACCATGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTGTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:1970299"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL"
                                                                                                                                                                                                                                                                                                                   GI:4442439
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                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                SOURCE
ORGANISM
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AI196154
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
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  TITLE
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AI196154.1
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                          1 (bases 1 to 605)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                 ui69d08.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1887663 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                              sequence.
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 4
Location/Qualifiers
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME185-FL3; Site_1: DraIII
(CACCATGTGTG); Site_2: DraIII (CACCATGTG); 1st Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME185-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI shoul
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
contracted to exclude fragments <1.5kb. Library
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| lab_host="DH10B"
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                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 380)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
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Seq primer:
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI785039
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EST.
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                             Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
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//clone lib="Sugano mouse liver mlia"
//note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
(CACCTGTGTG); Site 2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG); XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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/sex="female"
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Pred. No. 2.6e-13;
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Best Local Similarity
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                            333 CAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 367
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61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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CAGAGAGCTGTGACCACCATTGCCACTACTATCTA
                                                                                                 TCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCATACGGCCGTCTGCC
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                 /clone_lib="Sugano mouse liver mlia"
/clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACCATGTGTG); Site_2: DraIII (CACCATGTG); 1st Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
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constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rry sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dev_stage="adult"
lab_host="DH10B"
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'clone="IMAGE:1888018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                  22.1%;
91.6%;
                                                                                                                                                                                                                     Score 82.2; DB 1;
Pred. No. 1.7e-12;
                                                                                                                                                                                                Mismatches
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Maximum Match 10
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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seq length: 2000000000
         Gapop 10.0 , Gapext 1.0
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372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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/ Ggn2_6/ptodata/2/pubpna/USO9_FUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO9_FUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO9E_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO9C_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO9_FUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO9_FUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO9_FUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                           cgn2
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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76.4	154	219	219.4	223.6	321	372	Score	
20.5	41.4	58.9	59.0	60.1	86.3	100.0	Match	Query
1500	423	219	270	423	321	372	Match Length DB	
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US-09-917-800A-1608	US-09-972-916A-6	US-09-972-916A-2	US-09-972-916A-3	US-09-972-916A-6	US-09-972-916A-4	US-09-972-916A-5	Length DB ID	
Sequence 1608, Ap	Sequence 6 Appli	Sequence 2, Appli	Sequence 3, Appli	Sequence 6, Appli	Sequence 4, Appli	Sequence 5, Appli	Description	

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9.0	•		•	•	•	•	•	•	•	•	9.4	9.4	9.5	9.5	9.6	9.6	9.6	9.6	9.7	9.8	9.9	10.1	10.1	10.2	10.2	10.8	13.7	13.7	14.8	14.8	17.2	17.2	17.2	17.2	20.5	20.5	20.0
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US-10-719-993-35505	US-10-741-600-17905	US-10-741-601-5746	US-10-227-577-1270	US-10-091-504-1270	US-09-764-869-1270		US-10-091-504-1269	US-09-764-869-1269	US-10-767-701-15088	US-10-011-585A-76	US-10-027-632-164336	US-10-027-632-164336	US-10-739-930-5461	US-10-424-599-61023	US-09-918-995-22070	US-10-764-420-947	US-10-037-182-3	US-09-845-583-1	US-10-029-386-5186	US-10-094-749-9	US-10-264-237-828	US-10-017-122-1	US-10-029-386-20306	US-10-221-613-148	US-10-311-455-970	US-10-085-117-172	US-09-972-916A-3	_	US-10-152-319A-2150	US-10-388-934-36	US-10-893-315-160	US-10-893-315-126	8-10-756	07-23	S-10-152-31	US-10-191-803-73	-10-300-334-
3550	e 1790	Sequence 5746		Sequence 1270	1270,	1269	Sequence 1269	Sequence 1269,		Sequence 76,	Sequence 1643	Sequence 1643	Sequence 5461,				Sequence 3, A		Sequence 5186	Sequence 9, A	Sequence 828,	Sequence 1, A		Sequence 148,	Sequence 970,	ര		'				Sequence 126,	æ	quence :	equence 161:	e 73,	equence o, /
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ALIGNMENTS

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US-09-972-916A-5
                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 5
LENGTH: 372
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09972916A Patent No. US20020107198A1 GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
                                                                                                                                   Query Match 100.0%; Score 372; DB 9; I Best Local Similarity 100.0%; Pred. No. 2.5e-116; Matches 372; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                 FEATURE:
61 GGCCAGAGTCCAGGAACCACGGGAGTGCCCCCGTGCGCCCATGTACACTGGGGGCCAGAGT 120
                                              Н
                                                                         1 TACACTGGGGGCCAGAGTCCAGGAACCCACGGGAGTGCCCCCGTGCGCCCCATGTACACTGGG
                                              TACACTGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGG 60
                                                                                                                                                                                  Length 372;
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; OTHER INFORMATION: Synthesized
US-09-972-916A-4
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US-09-972-916A-4
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Patent No. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 4
LENGTH: 321
TYPE: DNA
ORGANISM: Artificial Sequence
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 301
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                                                                                                                                                                                 TATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCCGTGCTGCCGAG
                                                                                                                                                                                                                               TACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGG
CTTCCGCTACTAGCTAGCCGC
               CTTCCGCTACTAGCTAGCCGC 372
                                                    CAMACCCAGCGAGCATTGAACACTGCACACGCCATCTGCCCAGAGAGCTGTGACCACCA
                                                                             CAAACCCAGCGAGCATTGAACACTGCACACGCCATCTGCCCAGAGAGCTGTGACCACCA 351
                                                                                                        CCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACA
                                                                                                                                 CCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACA
                                                                                                                                                            TATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCGTGCTGCCGAG
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321
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US-09-972-916A-6
                                                                 GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
APPLICANT: Thule, CLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1992/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILLING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 6
LENGTH: 423
TYPE: DNA
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Patent No. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                     Sequence 3, Application US/09972916A Patent No. US20020107198A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                    LENGTH: 270
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76.2%;
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Pred. No. 9.6e-66;
0; Mismatches 74
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US-09-972-916A-2
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Sequence 6, Application US/09972916A
PATENT NO. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITI-
FILE REFERENCE: US 1292/01 (VA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
PILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
LENGTH: 219
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                                                                                                                                                                                                                                                                                                                                                                                       Matches 219;
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Best Local Similarity
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Best Local Similarity
Matches 220; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Rattus norvegicus
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                                                                                                                                                                                                                           CCACTGCCCGCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACCGGCCATCTGCCC 333
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                                                                                                                                                                               AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC 372
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                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     58.9%;
                  SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                     Score 219; DB 9; pred. No. 3e-64; 0; Mismatches
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Pred. No. 2.3e-64;
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APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR APPLICATION NUMBER: US 60/290,645
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                                                                                             SEQ ID NO 1608
LENGTH: 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1608, Application US/09917800A Patent No. US20020119462A1
GENERAL INFORMATION:
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APPLICANT:
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                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR PILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
                                                                                                                                         SOFTWARE: Patentin Ver.
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_013144
                                                                         TYPE: DNA
                                         ORGANISM: Rattus norvegicus
                           FEATURE:
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Castle, Arthur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Elashoff, Michael
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APPLICANT: CASTLE, Archur

APPLICANT: ELASHOFF, Michael

TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling

FILE REFERENCE: 44921-5090US

CURRENT APPLICATION NUMBER: US/10/191,803

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US 60/303,819

PRIOR APPLICATION NUMBER: US 60/305,623

PRIOR APPLICATION NUMBER: US 60/305,351

PRIOR APPLICATION NUMBER: US 60/369,351

PRIOR APPLICATION NUMBER: US 60/377,611

PRIOR APPLICATION NUMBER: US 60/377,611
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US-10-388-934-5
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Publication No.
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Best Local Similarity
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Publication No. US20040005547A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Rattus norvegicus (No. US20040005547Alway rat)
-10-388-934-5
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Best Local
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APPLICANT: PORTER, Mark
APPLICANT: JOHNSON, Kory
APPLICANT: HIGGS, Brandon
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CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 0205336.9
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 02015657.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Suter-Di
APPLICANT: Wolf, De
TITLE OF INVENTION:
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NUMBER OF SEQ ID NOS: 862
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FILING DATE:
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No. US20040014040A1
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   2002-05-06
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98.7%;
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98.7%;
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Pred. No. 1.9e-15;
0; Mismatches 1;
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Pred. No. 1.9e-15;
0; Mismatches 1;
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; OTHER INFORMATION: Genbank Accession No. NM_013144 US-10-152-319A-1613
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PRIOR FILLING DATE: 2001-06-13
PRIOR PELICATION NUMBER: US 60/298,925
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR APPLICATION NUMBER: US 60/303,808
PRIOR APPLICATION NUMBER: US 60/303,808
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,808
PRIOR FILING DATE: 2001-08-28
PRIOR FILING DATE: 2001-08-28
                                                                                                                                                                                                      Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 2221
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1613
LENGTH: 1500
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Publication No. US20040072160A1
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 73
  Matches
                                             Query Match
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APPLICANT: Castle, Arthur
APPLICANT: Elashoff
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/324,928
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILING DATE: 2001-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Higgs, Brandon
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                                                                                                                                   TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
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ORGANISM: Rattus norvegicus
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Local Similarity 98.
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Score 76.4; DB 18; Length 1500; Pred. No. 1.9e-15; 0; Mismatches 1; Indels 0;
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Pred. No. 1.
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APPLICANT: Horne, Darci T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

FILE REFERENCE: 44921-5028-W0

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/237,054

PRIOR PILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: PATENTIN OBJECTION OF SEQ ID NOS: 3950

SOFTWARE: PATENTIN OBJECTION OF SEQ ID NOS: 3950

LENGTH: 6128
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US-10-756-149-1484
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US-09-880-107-2393
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Sequence 1484, Application US/10756149

Publication No. US20050181375A1

GENERAL INFORMATION:

APPLICANT: Aziz, Natasha
APPLICANT: Zlotnik, Albert

TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/756,149

CURRENT FILING DATE: 2004-01-12
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Best Local Similarity
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ilarity 63.2%;
Conservative (
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Pred. No. 5.2e-11
0; Mismatches 7
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RESULT 13
US-10-893-315-126
(Sequence 126, Application US/10893315
; Sequence 126, Application US/10893315
; Publication No. US20050147987A1
; GENERAL INFORMATION:
   APPLICANT: VENTER, J. Craig et al.
   APPLICANT: VENTER, J. Craig et al.
   TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION.
   TITLE OF INVENTION: USES THEREOF
   FILE REFERENCE: CL000786
; CURRENT APPLICATION UMBER: US/10/893,315
; CURRENT APPLICATION NUMBER: 00/231,397
   PRIOR APPLICATION NUMBER: 60/231,397
                                                                                                                                                                                                                                                                                                                                 US-10-893-315-126
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; ORGANISM: Homo
US-10-756-149-1484
                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 2172
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 126
LENGTH: 9173
                                                                                                                                                                                                                                                            Matches 156;
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SEQ ID NO 1484
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 5818
                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                        1842 TCCTCCCACCAGCGGTTTGCGTAGGGCCTTGGGTGCACTAGCAAAACTTATTTTGA 190
                                                                                                                                             180 ACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCC------GTGCTGCCG 229
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                                                                         CACAAACCCAGCGAGCATTGAACACTGC-ACACGGCCATCTGCCCAGAGAGAGCTGTGACCA 348
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nilarity 63.2%;
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Pred. No. 5.2e-11;
0; Mismatches 72
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Pred. No. 5.7e-11;
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RESULT 15
US-10-388-934-36/c
US-10-388-934-36/c
; Sequence 36, Application US/10388934
; Publication No. US20040005547A1
; GENERAL INFORMATION:
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SEQ ID NO 160
SENGTH: 9174
TYPE: DNA
ORGANISM: Human
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Publication No. US20050147987A1
GENERAL INFORMATION:
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Best Local Similarity 63.2
Matches 156; Conservative
 SEQ ID
                               FILE REFERENCE: 21199
CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 02005336.9
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION.
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000786
CURRENT APPLICATION NUMBER: US/10/893,315
CURRENT FILING DATE: 2004-07-19
                                                                                                                                                                                                     APPLICANT: Boess, Franziska
APPLICANT: Suter-Dick, Laura
APPLICANT: Wolf, Detlef
SOFTWARE: PatentIn version 3.1 
EQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/231,397
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                    TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
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TYPE: DNA
; ORGANISM: Rattus norvegicus (No. US20040005547Alway rat)
US-10-388-934-36
                                                                                                          Query Match
Best Local Similarity
Matches 60; Conserv
3028 CGCCCATG 3021
                                                       3088 TGCCAACGGAAGCCTTGTACACTGGGGGCCCAGAGTCCCACGGAAGTGCCCCCGTG 3029
                                                                       35 TGCCCCGTGCGCCCATGTACACTGGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTG 94
                           95 CGCCCATG 102
                                                                                                                   Conservative
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Pred. No. 5.3e-08;
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Search completed: September 1, 2005, 16:44:30 Job time: 1085.43 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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Match Length
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    1202784 seqs, 818138359 residues
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US-08-945-140-1

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US-09-949-016-12957

US-09-949-016-12139

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US-09-949-016-1770-171097

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36, Appl
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117,05, Appl
117,10, Appl
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			Query M Best Lo Matches	
349 CCACTT 2074 CCGCTC	230 AGCCAGC 1962 CCTGTGC 290 CACAAAC 2018CAT	120 TCCA 1842 TCCT 180 ACAC 1902 ACAC	atch cal Simi 156;	
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355 2080	CTTTATA	ACCACGGG	17. 63. vative	2.8 8.8 2130 4 US- 22.6 8.8 907 4 US- 22.6 8.8 134008 4 US- 22.2 8.7 505 4 US- 22.2 8.7 601 4 US- 22.2 8.7 601 4 US- 22.2 8.7 601 4 US- 22.2 8.7 4447 2 US- 22.2 8.7 4447 3 US- 22.2 8.7 4447 3 US- 22.2 8.7 4447 3 US- 22.2 8.7 4344 4 US- 23.2 8.6 36180 4 US- 23.2 8.6 36181 4 US- 23.2 8.6 36181 4 US- 23.2 8.7 4348 4 US- 23.3 8.6 36181 4 US- 23.2 8.7 4348 4 US- 23.3 8.6 36181 4 US- 23.3 8.6 36180 4 US- 32.2 8.7 4447 3 US- 32.2 8.7 4447 3 US- 32.2 8.7 4447 3 US- 32.2 8.7 4447 4 US- 32.2
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	AGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGA AGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCAGCATGGTCCACTGGCCAGCAGCATGGTCCACACAGAGAGGCTGTGCCACACAGAGAGGCTGTGCCACACAGAGAGGCTGTGCCACAAACCACACAGAAGAGAGTGTAACCACAAACAA	ICCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTCACAAGCAAAACAAAC	Score 63.8; DB 4; Lo Pred. No. 2.2e-10; 0; Mismatches 72;	09-909-962A-6 09-909-962A-7 09-585-645A-65 09-949-016-13841 09-949-016-35650 09-949-016-35650 09-949-016-177809 09-92-540-1177 09-949-016-16824 09-949-016-16163 09-92-540-1177 09-949-016-16163 09-974-528-404 09-774-528-404 09-774-528-404 09-774-528-404 09-774-528-404 09-774-528-404 09-774-528-404 09-774-528-404 09-774-528-404 09-774-528-404 01 01
	GTCCACTGCCCGCCGAGA 289 CGGCCACCGCCATCC 2017 GGCCAGAGAGCTGTGACCA 348	CAAAACAACTTATTTGA 179	Length 9173; Indels 19; Gaps 3;	Sequence 6, Appli Sequence 7, Appli Sequence 65, Appl Sequence 13841, A Sequence 15639, A Sequence 35651, A Sequence 177809, Sequence 177809, Sequence 3, Appli Sequence 3, Appli Sequence 1177, Ap Sequence 1177, Ap Sequence 11745, A Sequence 16144, A Sequence 16163, A Sequence 10411, A Sequence 10411, A Sequence 404, App ASSOCIATED ASSOCIATED ASSOCIATED

RESULT 2 US-09-949-001-36 ; Sequence 36, Application US/09949001 ; Patent No. 6825336

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08945140 Patent No. 6309878
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 36
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL000789
CURRENT APPLICATION NUMBER: US/09/949,001
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/231,323
PRIOR APPLICATION NUMBER: 60/231,323
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CHEN, Ruihuan
APPLICANT: DOIRON, Bruno
APPLICANT: KAHN, Axel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 9174
             CLASSIFICATION: 514
PRIOR APPLICATION UMATA:
APPLICATION UMMBER: FR 95/04558
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: GLUCOSE-INDUCIBLE RECOMBINANT VIRAL TITLE OF INVENTION: VECTOR
                                                                                                                                                                                                                                           COUNTRY: UZIP: 19426
                                                                                            FILING DATE:
                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Rhone-Poulenc Rorer Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                 : 500 Arcola Road, Mailstop 3C43
Collegeville
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US-08-791-849A-14/c
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                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                               CLASSIFICATION: 800
PRIOR APPLICATION UNDER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WATTER M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Makoro MURASE et al.

TITLE OF INVENTION: Method for Increasing Storage
TITLE OF INVENTION: Lipid Content in Plant Seed
NUMBER OF SEQUENCES: 15
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TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: January 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 1.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 194 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: WO PCT/FR96/00560 FILING DATE: 12-APR-1996 ATTORNEY/AGENT INFORMATION: NAME: Savitzky Esq., Martin F. REGISTRATION NUMBER: 29,699 REFERENCE/DOCKET NUMBER: EX95002-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1
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              TYPE: nucleic acid STRANDEDNESS: doub
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ZIP: 20005
                                                                                                                                   TELEFAX:
                                                     LENGTH:
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Local Similarity 88.2%;
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linear
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Pred. No. 2.6e-08;
0; Mismatches 8;
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RESULT 6
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US-09-949-016-11786/c
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                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6812339
GENERAL INPORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11786
LENGTH: 15108
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Best Local S
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LOCATION:
LOCATION:
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                                                                                                                                        2417
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                                                                                                                                                            34 GTGCCCCGTGCGCCCATGTACACTGGGGGCCCAGAGTCCAGGAACCACGGGAGTGCCCCGGT 93
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                                                                                                       G 94
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                                                                                                                                                                                                           Conservative
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6284..6417, 6605..6920, 7191..7301, 7453..7664, 7818..7910,
9480..10162)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(3212..3218, 3766..3948, 5917..6008,
6152..6283, 6418..6604, 6921..7191, 7302..7452, 7665..7817, 7911..8077
9298..9479, 10163..10269)
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6152..6283, 6418..6604, 6921..7191, 7302..7452,
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88.2%;
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Pred. No. 0.015;
0; Mismatches 13;
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Pred. No. 1.7e-07;
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                                                                                                                                                                                                                                          Length 15108;
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GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walkez, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
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US-09-484-970B-138/c
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SEQ ID NO 138
LENGTH: 3054
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PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILLE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-01-03
PRIOR PILING DATE: 2000-01-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FRANSEQ for Windows
SEQ ID NO 17205
LENGTH: 15108
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6426186 336987.1CB1
                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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                                   62 GCCAGAGTCCAGGAACCACGGGAGTGCCCCG 92
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                                                                                                                                                                Score 36.6; DB 3; Pred. No. 0.11;
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Pred. No. 0.015;
0; Mismatches 13;
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; ORGANISM: Human
US-09-949-016-16965
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001307
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR TILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FastSEQ for Windows Version 4.0
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LOCATION: (1)...(35471)
OTHER INFORMATION: n = A,T,C or
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ACTGTGGGGACACCTCGCCTGCACCCACCTCCCCCCCAGCCCCCGAGCACTGTGGGG
                                          ACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGGG 61
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Pred. No. 0.56;
0; Mismatches
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
ITILE OF INVENTION INTH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
ITILE OF INVENTION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 00/241,755
PRIOR APPLICATION NUMBER: 60/21,756
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-08
INUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 1650
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US-09-949-016-14710
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PRIOR FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 10287-056001
CURRENT APPLICATION NUMBER: US/09/845,583A
CURRENT FILING DATE: 2001-04-30
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APPLICANT: Brunken, William Joseph
APPLICANT: Champliaud, Marie-France
APPLICANT: Hunter, Dale
TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
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TYPE: DNA
ORGANISM: Mus musculus
ORGANISM: Human
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Pred. No. 0.36;
0; Mismatches 67;
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US-09-949-016-12147/c
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US-09-949-016-15394
; Sequence 15394, Application US/09949016
; Patent No. 6812339
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US-09-949-016-15394
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                                     Sequence 12147, Application US/09949016
Patent No. 6812339
GEMERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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SOFTWARE: FBSTSEQ for Windows Version 4.0
SEQ ID NO 15394
LENGTH: 16520
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Matches 7
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Best Local
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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; Sequence 17361, Application US/09949016
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CLOO1307
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 17361
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Patent No. 6812339
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Best Local (
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Best Local Similarity 51.9%;
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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TYPE: DNA
ORGANISM: Human
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (1)...(767677)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
FEATURE:
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NAME/KS: misc_feature
LOCATION: (1)...(767677)
OTHER INFORMATION: n = A,T,C or
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                                                                                       ATCACGGGACTCCCTGCACCCCACAGTCCACACG 562308
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RESULT 15

US-09-949-016-19194/c

Sequence 19194, Application US/09949016

Patent No. 6812239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR PRICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 19194

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-19194
Search completed: September 1, 2005, 07:07:16 Job time: 123.652 secs
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Minimum DB
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ALIGNMENTS

LOCUS DEFINITION ACCESSION REFERENCE AUTHORS JOURNAL COMMENT VERSION
KEYWORDS
SOURCE
ORGANISM Ś 밁 5 밁 Ş RESULT 1
RATILGFZ ORIGIN FEATURES Query Match Best Local Similarity Matches 213; Conserva source 325 205 Unterman,T.G., Lacson,R.G., McGary,E., Whalen,C. and Goswami,R. Biochem. Biophys. Res. Commun. (1991) In press Original source text: Rattus norvegicus (strain Sprague-Dawley) male adult liver DNA. M84484.1 GI:204927
insulin-like growth factor.
Rattus norvegicus (Norway rat)
Rattus norvegicus M84484 RATILGFZ 1181 by Rattus norvegicus insulin-like Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. CCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC TCACAAGCAAAACAAACTTATTTTGAACACGGGGGATCCTAGCACGCTGCCCTGACAATCA TCACAAGCAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA (bases 1 to 1181) 50.2%; ilarity 99.5%; Conservative Location/Qualifiers 1. .1181 /tissue_type="liver" /dev_stage="adult" /organism="Rattus norvegicus" /mol_type="genomic DNA" /strain="Sprague-Dawley" /db_xref="taxon:10116" sex="male" Score 212.4; DB 1 Pred. No. 1.2e-48; 0; Mismatches 1 ਰੂ growth DB 10; DNA A linear facter gene 1; Indels Whalen, C. and Goswami, R.G Length 1181; fragment. ROD 27-APR-1993 <u>.</u> Gaps 942 384 882 264

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JOURNAL
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                                                                                  Eryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, F., Cardenas, V., Garter, K., Cavacos, I., Ceasar, H., Center, A., Chardo, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chu, J., Cheveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davis, C., Davis, C., Davys, C., Ding, Y., Dinh, H., Divya, K., Dragal, M.L., Davis, C., Davis, C., Davys, C., Ding, Y., Dinh, H., Divya, K., Dragar, H., Duyan, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Delgado, O., Denson, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Bscotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Bscotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Bscotto, M., Hernandez, J., Gall, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, B., Geer, K., Gill, R., Grady, M., Guerra, W., Guevarz, W., Gunaratine, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, M., Hernandez, J., Hernandez, J., Jackson, A., Johnson, B., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kally, S., Khally, S., Levan, J., Lewis, L., Li, Z., Liu, J., Lorensuhewa, L., Loulseged, H., Lovan, J., Lewis, L., Li, Z., Liu, J., Lorensuhewa, L., Colled, M., Martin, K., Martin, R., Mart
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                                                                          Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                      Unpublished
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Genome Sequencing Consortium
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8, *** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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NOTE: This is a "working draft" sequence. It currently consists of 63 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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Center clone name: CH230-97018

Center clone name: CH230-97018

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329

Consensus quality: 135613 bases at least Q40

Consensus quality: 140849 bases at least Q30

Consensus quality: 145680 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 1363)
Mohn,K.L., Waddle,J.R. and Taub,R.
Comparison of mouse and human IGFBP-1 genes reveals a potential
insulin-responsive sequence and conservation of all intron/exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee,J., Greenbaum,L., Haber,B.A., Nagle,D., Lee,V., Miles,V., Mohn,K.L., Bucan,M. and Taub,R. Structure and localization of the IGFBP-1 gene and its expression during liver regeneration Hepatology 19 (3), 656-665 (1994) 94164648
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964. .>1336
/codon_start=1
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/db_xref="GOA:P47876"
/db_xref="UniProt/Swiss-Prot:P47876"
                                                                                                                                                                                                                                                                                                               500.
                                                                                                                                                                                                          sequences"
                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                        /cell_line="NIH 3T3"
/cell_type="fibroblast"
/clone_lib="genomic, lan'
/dev stage="embryo"
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                                                                                                                                                                                                                                            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Apr 12, 2002 this sequence version replaced gi:19847866. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found ar
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AL607124
AL607124.15
                                                                                                                                     http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-20C9 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                       database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (11-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oliver, K.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murinae; Mus
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BC013345
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VERSION
                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
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                                                                                                                                             REMARK
                                                                                                                                                                                                                                                     JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                         Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Mang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, M.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Wadan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Wyers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                             NIH-MGC Project URL: http://mgc.
Contact: MGC help desk
                                                                                                                                                                                           Submitted (31-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1569)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC013345 Insulin-like growth factor binding protein (CDNA clone MGC:14075 IMAGE:4161889), complete cds.
                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                            Strausberg, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC013345
BC013345.1
                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                   12477932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAGAGCTGTGACCACCATTGCCACTACTATCTA
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                                                                                                                                                                                                                                                                                                                                      (bases 1 to 1569)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:15426482
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Pred. No. 5.7e-42;
                                                                                                                                                                                                                                                                                                                                                                                             U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                          .nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 192843;
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ACCESSION
VERSION
KEYWORDS
                                                                                                                           SOURCE
ORGANISM
                                                                                                                                                                                                                                                                     RESULT 6
AY560836
                                                        REFERENCE
                                                                                                                                                                                                                                    DEFINITION
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                    AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103;
                                                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                                                                   20
 Li,Y., Klimanis,D. and Hallenbeck,J.M.
Cloning and characterization of insulin-like growth factor binding protein 1 (IGFBP-1) from thirteen-lined ground squirrel
                                                                                    Spermophilus tridecemlineatus (thirteen-lined ground squirrel)
Spermophilus tridecemlineatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurin
                                                                                                                                                                                                  1507 bp Spermophilus tridecemlineatus ir protein 1 (IGFBP1) mRNA, complet AY560836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 18 Row: 1 Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
                                                                     Spermophilus.
                                                                                                                                                                                 AY560836.1 GI:45505308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Madan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 92.8
03; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                     CACACGGCCATCTGCCCAGAGAGCTGTGACCACCACCTTCCGCTACTAGCTA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTG
                                                                                                                                                                                                                                                                                                                                            CACACGGCCGTCTGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 130
                                                                                                                                                                                                                                                                                                                                                                                                                     TGGGCAGCCAGCATGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTG
                                                      (bases 1 to 1507)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="insulin-like growth factor binding protein 1"
/protein_id="AAH13345.1"
/db_xref="GLG483"
/db_xref="GLG483"
/db_xref="HGG196436"
/translation="MPEFLTVUSWPFLILLSFQIGVAAGAPQPWHCAPCTAERLGLCP
PVPASCPEISRPAGGGCCPTCALPMGAACGVATARCAQGLSCRALPGEPRPLHALTRG
GCACVPEPAAPATSTLSSSQHEEAKAAVVSADELSESPEMTEEQLLDSFHLMAPSRED
OPILMWANISTYSSMRARBIADLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNKNGFYHSKQCETSLDGEAGLCWCVYPWSGKKIPGSLETRGDPNCHQYFNVHN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="synonym: IGFBP-1"
/db_xref="LocusID:16006"
/db_xref="MGI:96436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Liver, normal.
/clone_Tib="NCI_CGAP_Li9"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         )
mol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="Igfbp1"
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/clone="MGC:14075 IMAGE:4161889"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.2%;
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from thirteen-lined ground
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                     complete
                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                  ng mRNA
                                                                                                                                                                                                                     cds.
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growth factor
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equirrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                male mouse."
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actor binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                              Mendrick,D.,
Elashoff,M.R.
                                                                                                                                            Gene Logic,
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Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Sequence 1608 from Patent WO0210453.
AX401932
AX401932.1 GI:21338112
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                                                                                                                                                            Molecular toxicology modeling Patent: WO 0210453-A 1608 07-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li,Y., Klimanis,D
Direct Submission
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Y., Klimanis, D. and Hallenbeck, J.M
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/organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/mol_type="taxon:10116"
/db xref="taxon:10116"
/note="EMBL/GenBank Accession No. NM_013144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="insulin-like growth factor binding
/protein_id="AAS67029.1"
/db_xref="GI:45505309"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Spermophilus
/mol_type="mRNA"
/db_xref="taxon:43179"
                                                                                                               location/Qualifiers
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67.6%;
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RATIGFB
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AX827271
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Best Local Similarity
Matches 77; Conserv
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Patent:
F. HOFFM
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Sequence 5
AX827271
                                                                 1 (bases 1 to 1500)
Mohn,K.L., Melby,A.E., Tewari,D.S., Laz,T.M. and Taub,R.
The gene encoding rat insulinlike growth factor-binding
is rapidly and highly induced in regenerating liver
Mol. Cell. Biol. 11 (3), 1393-1401 (1991)
                                                                                                                                          Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                  8
                                   Original
                                                                                                                                                                             M58634.1 GI:204732
IGF binding protein-1.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                  M58634
                                                                                                                                                                                                                            RATIGFB mRNA 1500 bp mRNA RATIGFB binding protein-1 (rIGFBP-1) mRNA
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                                                                                                                                                                                                                                                                                                                CACTTCCGCTACTAGCTA 418
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                                   source text:
1. .1500
/organism="Rattus norvegicus"
       Location/Qualifiers
1. .1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
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from Patent EP1344834.
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98.7%;
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Rodentia;
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Pred. No. 1.5e
0; Mismatches
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Pred. No. 1.5e-10;
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Sciurognathi; Muridae;
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mat_peptide
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61
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                                                                                                                                                                                                                                                                               Gould-Rothberg, B.E., Dipippo, V.A., Ramseh, T.M. and Gerwein, R.W. Method of identifying toxic agents using nsaid-induced differential gene expression in liver patent: WO 0138579-A 46 31-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 46
AX163782
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                                                                                                                                                                                                                                                                Patent: WO 0138579-A 46 31-MAY-2001;
Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Norway
                                                                                                                                                                                                                                                                                                                                                                                                                                                AX163782.1
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CACTICCGCTACTATCTA 78
                  CACTTCCGCTACTAGCTA 418
                                                         CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
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                                                                                                                   Conservative
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235. .975
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                                                                                                                                                                                       /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                   Location/Qualifiers
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/protein_id="AAA41380.
/db_xref="GI:204733"
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/strain="Fisher"
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                                                                                                                              18.1%;
98.7%;
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                                                                                                                  Score 76.4; DB 6;
Pred. No. 1.5e-10;
0; Mismatches 1
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Pred. No. 1.5e-10;
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RESULT 11 RATIGFBA

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On Nov 30, 1995 this sequence version replaced gi:385167.
Original source text: Rattus norvegicus (strain Sprague-I
DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 5001)
1 (bases 1 to 5001)
Lacson,R., Oehler,D., Yang,E., Goswami,R. and Unterman,T. Dideoxy sequencing and structural analysis of the rat ins growth factor binding protein-1 gene Blochim. Biophys. Acta 1218 (1), 95-98 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus.
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Mammalia; Eutheria; Rodentia; Sciurognațhi; Muridae;
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L22979
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                                                                   Similarity
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                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="IGFBP-1"
join(153. .525,1850. .
/gene="IGFBP-1"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                        PVPASCPEISRPAGCGCCPTCALPLGAACGVATAACAQGLSCRALPGEPRPLHALTRG
QGACVLEPAAPATSSLSGSQHEEAKAAVASEDELAESPEMTEEQLLDSFHLMAPSRED
QPILMNAISTYSSMRAREITDLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
                                                                                                                                                                                                               3003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="insulin-like growth factor binding protein"
/protein_id="AAA82581.1"
/db_xref="Gi:1098473"
/translation="MPEFLTVVSWPFLILLSFQVRVVAGAPQPWHCAPCTAERLELCP
                                                                                                                                                                                                                                                                                           /gene="IGFBP-1"
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                                                                                                                                                                                                                                                                                                                                          /gene="IGFBP-1"
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/dev_stage="adult"
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/db_xref="taxon:10116"
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/mol_type="genomic DNA"
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                                                                                                                                                 number=4
                                                                                                                                                                              number=3
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gene="IGFBP-1"
                                                                                                                                                                                                                               'number=3
                                                                                                                                                                                                                                              'gene="IGFBP-1"
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98.7%;
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                                                Score 76.4; DB 10;
Pred. No. 1.5e-10;
0; Mismatches 1;
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Klausner, R.D. Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Dlatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Fahey, J., Helicon, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Mitting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Schmutz, J., Myers, R.M., Butterfield, S.S., Krzywinski, M.I., Skalaka, U., Smailus, D.E., Generation and initial analysis of more than 15,000 full-length human and monuse CNNA segmence.
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                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 184 Row: e Column: 23
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Express Genomics CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing Genome at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Howard Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Director MGC Project.

Direct Submission

Submitted (02-AUG-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.
Dickson, M., Schmutz, J., Grimwood, J., Rodri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human and mouse cDNA sequences
broc. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                             равsed the following selection criteria: matched mRNA gi: 6981079
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/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
                                                                                                                                               Location/Qualifiers
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Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1510 bp
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SOURCE
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AY095345
LOCUS
                                                                                                                                                                                    FEATURES
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Submitted (11-APR-2002) Department of Obstetrics and Obstetri
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Papio anubis insulin-like growth factor binding
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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/db_xref="LocusID:25685"
/db_xref="RATMAP:44422"
/db_xref="RGD:2872"
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                                                     /organism="Papio anubis'
/mol_type="genomic DNA"
/db_xref="taxon:9555"
/gene="IGFBP-1"
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/clone_lib="NIH_MGC_236"
/lab_host="DH10B"
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IGFBP1 X1.
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Primer A: TGCACTAGCAAAACAAACTT
                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 448)
Cox,D.G., Boillot,C. and Canzian,F.
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                           Fax: +33-4-72738388
                                                                                                                                                                                                                                                           Tel: +33-4-72738698
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150, cours Albert-Thomas,
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/protein_id="AAM23273.1"
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Search completed: September 1, 2005, 03:27:00 Job time : 2637.79 secs

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AI52939 ui87c09.y
CA478518 AGENCOURT
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ALIGNMENTS

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AUTHORS
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Matches 103; Conserv
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National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyce Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLAM9443 row: j column: 02

High quality sequence stop: 581.

Location/Qualifiers

1 1013
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to,1013)
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    Conservative
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/clone="IMAGB:4161889"
/clone=IMAGB:4161889"
/clone_lib="NCI CGAP_Li9"
/clone_lib="NCI CGAP_Li9"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
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                      23.2%;
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  Score 98.2; DB 2;
Pred. No. 3.7e-17;
0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia Genome Res. 13 (6B), 1273-1289 (2003)
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BY783538 RIKEN full-length enriched, 17.5 days embryo Mus musculus cDNA clone L930176D05 5', mRNA sequence.
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                                                                                               ATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATC 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      visit our web site (http://genome.gsc.riken.jp/) for
                                                                                                                                                                                                                                                                                          tissue_type="whole body"
/dev_stage="17.5 days embryo"
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                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
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Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY794229 331 bp mRNA linear E
BY794229 RIKEN full-length enriched, 17.5 days embryc
Mus musculus cDNA clone L930292H24 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepare mouse tissues
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TGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 100
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                                                                                                                                   ATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATC
                                                 TGCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 418
                                                                                                   ATGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTC 61
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                                                                                                                                                                                                  Conservative
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/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                               clone="L930292H24"
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92.9%;
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Sciurognathi;
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1, 17.5 days embryo whole body
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thi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                62
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Mus musculus
Mus musculus
       AI785818
401 bp mRNA linear EST 02-ui78h05.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1888569 5' similar to gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: roome Exploration Contact: Republic Contact: Republic Contact: Con
                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci, P., Waki, K., Shiraki, T., Konno, H., Shibata, K., Itoh, M., Alzawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S., Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watahiki, A., Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A., Kusakabe, M., Gustincich, S., Beisel, K., Pavan, W., Aldinis, V., Nakagawara, A., Held, W. A., Iwata, H., Kono, T., Nakauchi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M., Hensch, T.K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P., Muramateu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y. Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia Genome Res. 13 (6B), 1273-1289 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
AI785818
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1 (bases 1 to 354)
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/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
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/mol_type="mRNA"
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EN full-length enriched, 17.5 days embryo whole body
cDNA clone L930052G15 5', mRNA sequence.
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AUTHORS
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AI196314

10171-2071-71 Sugano mouse liver mlia Mus musculus CDNA clone 1174-2071-71 Sugano mouse liver mlia Mus musculus CDNA clone IMAGE:1887828 5' similar to gb:M59316 rani INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HŪMAN); gb:X81579 M.musculus FACTOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91;
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The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 401)
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This clone is available royalty-free through LLNL; contact the
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Fax: 314 286 1810
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Location/Qualifiers
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//note="Organ: liver; Vector: pMEISS-FL3; Site 1: DraIII
(RACTGTGTG); Site_2: DraIII (CACCATGTG); lst Etrand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pMEISS-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/strain="C57BL"
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Pred. No. 5.7e-14;
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AI530146 706 bp mRNA linear EST 18-MAR-1999 ui89f09,1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1889609 5' similar to gb:m59316 rnal INSULIN-LIKE GROWTH PACTOR BINDING PROTEIN 1 PRECURSOR (HŪMAN); gb:x81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 480)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuo, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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AI196314.1 GI:3748920
EST.
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The WashU-HHMI Mouse EST Project
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
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/strain="C57BL"
/db_xref="taxon:10090"
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92.9%;
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Pred. No. 5.9e-14;
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A1098594 "MANN LEARN TO BE WAVE THE THE THREE TH
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Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptce, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R. Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R., Waterston, C. Malleon, R., Waterston, C. Mouse EST Project 1999

The WashU-NCI Mouse EST Project 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
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/Glone liber Sugano mouse liver pMEI8S-FL3; Site 1: DraIII
/noter Torgan: liver; Vector: pMEI8S-FL3; Site 1: DraIII
(CACCATGTG); Site 2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pMEI8S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI shou
be used to isolate the cDNA insert. Size selection was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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/mol_type="mRNA"
/strain="C57BL"
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'clone="IMAGE:1889609"
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Pred. No. 6.4e-14;
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RESULT 9
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Best Local (
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JOURNAL
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Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 314 600 1000
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubudesel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 765)
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EST.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Sugano mouse liver mlia"
//note="Organ: liver; Vector: pME18S-FL3; Site 1: DrallI
(CACCATGTG); Site_2: DrallI (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DrallI adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DrallI sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). Xhol should
be used to isolate the cDNA insert. Site selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTGTCTGCTTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/clone="IMAGE:1481988"
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/strain="C57BL"
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92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                 Score 86.8; DB 1
Pred. No. 6.5e-14
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A1529939
799 bp mRNA linear EST 18-MAR-19 ui87C09, yl Sugano mouse liver mlia Mus musculus CDNA clone IMAGE:1889392 5' similar to gb:m59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:K81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
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Fax: 314 286 1810
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/note="Organ: liver; Vector: pME185-FL3; Site 1: DraIII
(CACCMTGTG); Site_2: DraIII (CACCMTGTG); lst Strand cDNA
was primed with an oligo(dT) primer
[ANCTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME188-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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lab_host="DH10B"
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strain="C57BL"
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92.9%;
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Pred. No. 6.6e-14;
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clone
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         AGENCOURT 10789306 NIH MGC_152 Mus musculus cDNA clone IMAGE:6766752 5', mRNA sequence.
CA478518
CA478518.1 GI:24936188
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The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:973716
Seq primer
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                              GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA
                                                                                                                                                                                                                                                                                                                       TGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="Sugano mouse liver mlia"
//note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
//note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
(CACCTGTGTG); Site 2: DraIII (CACCATGTG); lst Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
conservated by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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Location/Qualifiers
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/clone="IMAGE:1889392"
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/lab_host="DH10B"
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Pred. No. 6.6e-14;
0; Mismatches 7;
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                                                                                                                                                                                                                                                       uk28b10.y1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1970299 5' similar to gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA sequence.
Unpublished (1999)
            Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylle, Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., SchuRitter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCan Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 848)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Mark Bittinger
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLKM000138 row: m column: 23
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1 (bases 1 to 811)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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                                                                                                                                                                     Mus musculus
                                                                                                                                                                                       Mus musculus (house mouse)
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Tissue Procurement: Bradfield Laboratory
                                                                                                                                                                                                                          AI790802.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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Rodentia;
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Pred. No. 6.6e-14;
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                                                    Cardenas, M., McCann, R.,
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Best Local S
Matches 91
                               TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 852)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Other_ESTs: uk28b10.x1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:987039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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/lab_host="DH108"
/clone lib="Sugano mouse kidney mkia"
/note="Organ: kidney; Vector: pME183-FL3; Site_1: DraIII
/note="Organ: kidney; Vector: pME183-FL3; Site_1: DraIII
(CACCTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME188-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI shoul
be used to isolate the CDNA insert. Size selection was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
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/strain="C578L"
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Pred. No. 6.7e-14;
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                           TITLE
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Best Local Similarity
                                                                                                                                                                                                                                              AUTHORS
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By mRNA linear EST 14-OCT-15 usigned by linear linea
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                                                                                              Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 605)
                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
This clone is available royalty-free through LLNL;
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
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Fax: 314 286 1810
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                  WashU-HHMI Mouse EST Project
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//Clone lib="Sugano mouse liver mlia"
//Clone lib="Sugano mouse liver mlia"
//Clone libe" Vector: pmBIBS-FL3; Site 1: DraIII
(CACCTGTGG); Ist Etrand cDNA
was primed with an oligo(dT) primer
[ATCTGGCCTTTTTTTTTTTTTTTTTT], double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pmE18S-FL3
vector (5' site CACCTGTGG, 3' site CACCTAGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
conserructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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Pred. No. 6.7e-14
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EST 14-OCT-1998

Dubuque, T.

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Gaps

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REFERENCE
AUTHORS
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AI785039
                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 TGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
1 (bases 1 to 380)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

The Washlu-NCI Mouse EST Project 1999

Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                   ui73a06.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1888018 5' similar to gb:X81579 M.musculus mRNA for
insulin-like growth factor binding (MOUSE);, mRNA sequence
                                                                                                                                                                                                                                       Mus musculus (house mouse)
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                          AI785039.1 GI:5332755
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:971987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCCAGAGAGCTGTGACCACCACCTTCCGCTACCTAGCTA 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /notes Torgan: liver; Vector: pME18S-FL3; Site 1: DraIII (CACTGTGTG); Site 2: DraIII (CACCATGTG); lst strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTTTTTTT] double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
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/sex="female"
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/strain="C57BL"
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91.8%;
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Pred. No. 1.8e-13;
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Search completed: September Job time: 3217.09 secs

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                                                                                                                                                                                                                    Local Similarity
                              384 CAGAGAGCTGTGACCACCACCTTCCGCTACTAGCTA 418
                                                                                                                          324 TCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCC 383
61
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Other ESTs: ui73a06.x1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                 TCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCATACGGCCGTCTGCC
CAGAGAGCTGTGACCACCATTGCCACTACTATCTA
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                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                /clone_lib="Sugano mouse liver mlia"
//clone_lib="Sugano mouse liver mlia"
//note="Organ: liver; Vector: pMEJBS-FL3; Site 1: DraIII
/(CACCATGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT], double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pMEJBS-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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Location/Qualifiers
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/lab_host="DH10B"
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/clone="IMAGE:1888018"
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/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
                                                                                                                                                                                                                 19.4%;
91.6%;
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Pred. No. 1.2e-12;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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423
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Published Applications NA:*

Published Applications NA:*

Published Applications NA:*
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/cgn2_6/ptodata/2/pubpna/VSO6_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9A_PUBCOMB.seq:*
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US-10-363-483A-40664	0-363-483A-4066	-10-363-345A-4066	-10-363-345A-406	-10-719-993-3550	-10-719-993-3	-10-764-420-94	-10-037-182-	09-845-583-	-10-719-9	-10-719-993-3550	-10-741-600-6	-10-085-117-1	-10-756-149-	-263-3	-10-461-668-1	-10-096-399A	-10-09	US-10-363-483A-40660	-10-363-483A-406	-10-363-345A-4066	-10-363-345A-4065	72-916A-6	-10-741-600-17)29-386-		-10-029-386-	09-972-916	-10-152-31	-10-388-93	-10-893-31	-10-893-	S-10-756-14	09-880-107	US-10-152-319A-1613	-10-191-803-	US-10-388-934-5	US-09-917-800A-1608
Sequence 40664, A	•	4066	Φ	e 35509,	e 35504	equence 94	e 3	Sequence 1, Appli	e 6865,	equence 35505	69952	e 172,	4571,	381,	11, 7		11,	4066	40659,	40660	e 40659,	•	17972	516	껕	e 203	: A	e 2150,	equence 36,	160,	equence 126,	Φ	2393,	1613, A	e 7	ce 5, 1	9

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US-09-972-916A-6
                                                                                                                                       Query Match
Best Local S
Matches 423
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                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 6
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Thule, Peter M.

TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION PILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR APPLICATION NUMBER: US 60/239,113
                                                                                                                                                                                                                                                                                                                               LENGTH: 423
TYPE: DNA
                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                       / Match 100.0%; Score 423; DB 9; Length 4:
Local Similarity 100.0%; Pred. No. 2.2e-136;
les 423; Conservative 0; Mismatches 0; Indels
  61
                                                                                   1 CATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTACATGGGCGC 60
ACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTACATGGGCGCACGGGGCAC 120
                                                 CATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTACATGGGCGC 60
                                                                                                                                                                                     Length 423;
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Score

Match Length DB

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270 223.6 219.4 219 154

100.0 63.8 52.9 51.9 51.8 36.4

423 270 372 321 219 372 372

US-09-972-916A-6 US-09-972-916A-3 US-09-972-916A-6 US-09-972-916A-4 US-09-972-916A-2 US-09-972-916A-6 US-09-972-916A-6

> Sequence Sequence Sequence

Sequence

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Sequence Sequence Sequence

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Sequence 3, Application US/09972916A

Patent No. US20020107198A1

Patent No. US20020107198A1

Patent No. US20020107198A1

Patent No. US20020107198A1

GENERAL INFORMATION:

APPLICANT: Thule, Peter M.

FILE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF

FILE REFERENCE: US 1292/01 (VA)

CURRENT APPLICATION NUMBER: US/09/972,916A

CURRENT FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/239,113

PRIOR APPLICATION NUMBER: US 60/239,113

PRIOR FILING DATE: 2000-10-11

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 3

LENGTH: 270
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US-09-972-916A-3
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Best Local S
Matches 270
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                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                   334
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 241
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            TGACCACCACTTCCGCTACTAGCTAGCCGC 423
                                                          AAACAAACTTATTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCGT
                                                                                                                                                              AAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCGT
 TGACCACCACTTCCGCTACTAGCTAGCCGC
                                                                                                               CATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTATCACAAGCA
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                                                                                                                                                                                                                                  63.8%; Score 270; DB 9; ilarity 100.0%; Pred. No. 2.7e-83; Conservative 0; Mismatches 0;
270
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US-09-972-916A-4

Sequence 4, Application US/09972916A Patent No. US20020107198A1

GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILLING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 4
LENGTH: 321
TYPE: DNA
ORGANISM: Artificial Sequence

FEATURE:

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US-09-972-916A-5
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Patent No. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT TILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 5
LENGTH: 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 297; Conserv
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343
                               394
                                                                    283
                                                                                     334 GCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTG 393
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                                 TGACCACCACTTCCGCTACTAGCTAGCCGC 423
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                                                                    GCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTG
                                                                                                                                        AAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCGT
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Pred. No. 3.9e-67;
0; Mismatches 74;
372
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RESULT 6
US-09-972-916A-5/c.
Sequence 5, Application US/09972916A
; Patent No. US20020107198A1
; GENERAL INFORMATION:
; APPLICANT: Thule, Peter M.
; TITLE OF INVENTION: GLUCOSE SENSITIVE RE
; FILE REFERENCE: US 1292/01 (VA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09972916A
Patent No. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLICCOSE SENSITIVE REGULATOR OF
FILE REFERRICE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
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US-09-972-916A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
LENGTH: 219
TYPE: DNA
ORGANISM: Rattus norvegicus
PEATURE:
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                      Matches 219; Conservative
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                                                                                                                                                                                                         CCACTGCCGGCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
                                                                                                                                                                                                                                      CCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
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100.0%; Pred. No. 1.3e-65;
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Pred. No. 1.1e-65;
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                   INSULIN TRANSCRIPTION
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; Sequence 4, Application US/09972916A
; Patent NO. US20020107198A1
; GENERAL INPORMATION:
; APPLICANT: Thule, Peter M.
; TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF FILE REFERENCE: US 1292/01 (VA)
; CURRENT APPLICATION NUMBER: US/09/972,916A
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/239,113
; PRIOR PILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 6
RESULT 8
US-09-917-800A-1608
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                                                                                                                                                                                                                                                                                                                                                                            ; SEQ ID NO 4
; LENGTH: 321
; TYPE: DNA
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CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 5
LENGTH: 372
                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                          Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Synthesized
                                                                                                                                                                                                                                              Local Similarity
                                                                                              111 CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 153
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                                                                         43
                                                                                                                                                                    51 ACATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTACATGGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 ACATGGGCGCACGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTACATGGGCG
                                                                         CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 1
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                                                                                                                                                                                                                                                                                                                   Synthesized
                                                                                                                                                                                                                      24.3%; Score 103; DB 9; 100.0%; Pred. No. 2.9e-25; tive 0; Mismatches 0;
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Sequence 1608, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur

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RESULT 9
US-10-388-934-5
                                                        ; LENGTH: 1500
; TYPE: DNA
; ORGANISM: Rattus norvegicus (No. US20040005547Alway rat)
US-10-388-934-5
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SEQ ID NO 1608
LENGTH: 1500
Query Match
Best Local Similarity
                                                                                                                                      SEQ ID NO 5
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                                                                                                                                                                                                                             FILE REFERENCE: 21199
CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 02005336.9
PRIOR FILING DATE: 2002-03-14
PRIOR FILING DATE: 2002-03-14
                                                                                                                                                      PRIOR APPLICATION NUMBER: 02015657.6
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
SOFTWARE: PatentIn version 3.1
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APPLICANT: Suter-Dick, Laura
APPLICANT: Wolf, Detlef
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PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
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TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
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ORGANISM: Rattus norvegicus
FEATURE:
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FILING DATE: 2001-06-06
APPLICATION NUMBER: US 60/297,457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/292,336 FILING DATE: 2001-05-22
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98.7%;
18.1%;
98.7%;
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Pred. No. 7.9e-16;
0; Mismatches 1
Score 76.4; DB 17; Pred. No. 7.9e-16;
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                  Length 1500;
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APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Higgs, Brandon
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT APPLICATION STATES (1982)
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US-10-152-319A-1613
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CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,819
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/305,623
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: US 60/377,611
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 1140
COMMENDED. DEFORTS VICES OF SERVING SERVINGS SERVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-191-803-73
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1613, Application US/10152319A
Publication No. US20040072160A1
GENERAL INFORMATION:
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Publication No. US20040014040A1
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APPLICANT: CASTLE, Arthur
APPLICANT: ELASHOFF, Michael
TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
FILE REFERENCE: 44921-5090US
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APPLICANT: PORTER, Mark
APPLICANT: JOHNSON, Kory
APPLICANT: HIGGS, Brandon
PRIOR APPLICATION NUMBER: US 60/292,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_013144
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77; Conserv
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Pred. No. 7.9e-16;
0; Mismatches 1;
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APPLICANT: Vockiey, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
FIGURIT: Scherf, Uwe
APPLICANT: Scherf, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
NUMBER OF SEQ ID NOS: 3950
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                                                                   ; OTHER INFORMATION: US-09-880-107-2393
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SEQ ID NO 1613
LENGTH: 1500
TYPE: DNA
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Best Local S
Matches 77
                                                                                                                                       SOFTWARE: PatentIn Ver.
SEQ ID NO 2393
LENGTH: 6128
TYPE: DNA
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 Query Match .
Best Local Similarity
Matches 141; Conserv
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PRIOR APPLICATION NUMBER: US 60/330,867
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                                                                                                       ORGANISM: Homo sapiens FEATURE:
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R APPLICATION N
FILING DATE:
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APPLICATION NUMBER: US 60/303,810
FILING DATE: 2001-07-10
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APPLICATION NUMBER: US 60/330,462
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o. US20020142981A1
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   Conservative
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 Score 60.8; DB 9; Pred. No. 3.1e-10; 0; Mismatches 52;
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Pred. No. 7.9e-16;
0; Mismatches 1
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                                Length 6128;
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; ORGANISM: Homo
US-10-756-149-1484
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US-10-756-149-1484
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Sequence 126, Application US/10893315
Publication No. US20050147987A1
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND TITLE OF INVENTION: USES THEREOF FILE REFERENCE: CL000786
CURRENT APPLICATION NUMBER: US/10/893,315
CURRENT APPLICATION NUMBER: US/10/893,315
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR FILING DATE: 2000-09-08
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CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1484
LENGTH: 6128
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Best Local Similarity
Matches 141; Conserv
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APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
FILE REFERENCE: file
                                                                                                                                                                                                                                                                                                                                   645
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Pred. No. 3.1e-10;
0; Mismatches 52;
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Sequence 160, Application US/10893315
; Publication No. US20050147987A1
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
    TITLE OF INVENTION: USES THEREOF
    FILE REFERENCE: CLO00786
; CURRENT APPLICATION NUMBER: US/10/893,315
; CURRENT APPLICATION NUMBER: 60/231,397
pRIOR APPLICATION NUMBER: 60/231,397
pRIOR RILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2172
; SOFTMARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 9174
; Type: DNA
; ORGANISM: Human
US-10-893-315-160
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US-10-893-315-160
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 126
LENGTH: 9173
TYPE: DNA
ORGANISM: Human
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Best Local Similarity
Matches 141; Conserv
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Search completed: September 1,

2005, 16:44:32

Job time : 1233.96 secs

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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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9.5 15108
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US-09-949-016-17205
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ALIGNMENTS

US-09-949-001-30 RESULT 1

Sequence 30, Application Patent No. 6825336 GENERAL INFORMATION:
APPLICANT: VENTER, J.

Application US/09949001

, APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
; FILER REPERENCE: CL000789
; CURRENT APPLICATION UNUMBER: US/09/949,001
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/231,323
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
SECTIMARE: FastSEQ for Windows Version 4.0

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RESULT 2
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; ORGANISM: Human
US-09-949-001-30
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Sequence 36, Application US/09949001
Sequence 36, Application US/09949001
Patent No. 6825336
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL000789

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RESULT 3
US-08-945-140-1
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SEQ ID NO 36
LENGTH: 9174
TYPE: DNA
                                              FILING DATE:

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION UNMBER: FR 95/04558

FILING DATE: 14-APR-1995

PRIOR APPLICATION UNMBER: WO PCT/FR96/00560

APPLICATION NUMBER: WO PCT/FR96/00560

FILING DATE: 12-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: SAVILZKY ESG., MARTIN F.

REGISTRATION NUMBER: 29,699

REGISTRATION NUMBER: 29,6909-US
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Best Local Similarity 66.5%;
Matches 141; Conservative
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CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/231,323
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: CHEN, Ruihuan
APPLICANT: DOIRON, Bruno
APPLICANT: KAHN, Axel
                  REFERENCE/DOCKET NUMBER: EXTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GLUCOSE-INDUCIBLE RECOMBINANT VIRAL TITLE OF INVENTION: VECTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1937 TAACCTCCTGGTGCAAGTGGCGCGGCCTGTGCCCCTTTATAAGGTGCGCGCTGTGTCCAGC 1996
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Pred. No. 2e-09;
0; Mismatches 52;
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Best Local Similarity
Matches 60; Conserv
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Makoto Flow.... APPLICANT: Makoto Flow.... Method for Increasing --
TITLE OF INVENTION: Lipid Content in Plant Seed
TITLE OF INVENTION: Lipid Content in Plant Seed
                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 13011 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                    FEATURE
                                                                  ORIGINAL SOURCE: ORGANISM: rat
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/791,849A FILING DATE: January 30, 1997 CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                     MOLECULE TYPE:
                                                                                                     NTI-SENSE:
 NAME/KEY:
LOCATION:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                     TOPOLOGY:
                                                                                                                                                   STRANDEDNESS:
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TELEFAX:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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o. 5914449
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805 Fifteenth Street, N.W., #700
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join(3212..3218, 3766..3948, 5917..6008, 6152..6283, 6418..6604, 6921..7191, 7302..7452, 7665..7817, 7911..8077
                                 SGD
                                                                  rat (Rattus norvegicus)
                                                                                                                                                                                                                                                                        202-371-8850
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                                                                                                                     DNA (genomic)
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Pred. No. 2.4e-08;
0; Mismatches 8;
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RESULT 6
US-09-949-016-12147
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US-09-949-016-16965
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                                                                                                                                                                                                                                                                                                                                           Query Match 10.6%;
Best Local Similarity 51.5%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOPTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 16965
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Patent No. 6812339
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Best Local (
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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LOCATION:
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                                                                                                   TGGACTCTGGCCCCCAGTGT
                                                                                                                                                                                                        GGGGAGGGAGGTGCAGGCGAGGTGTCCCCACAGTGCTCAGGGGGCTGGGGGAAGGGA
                                                                                                                                   AGGCGAGGTGTCCCCACAGT
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6284..6417, 6605..6920, 7191..7301, 7453..7664, 7818..7910,
9480..10162)
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6152..6283, 6418..6604, 6921..7191, 7302..7452,
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                                                                                                                                                                                                                                                                                                                                           Score 44.8; DB 4;
Pred. No. 0.00073;
0; Mismatches 97;
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Pred. No. 1.6e-07;
0; Mismatches 8;
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OF DETECTION AND USES THEREOF
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                                                                                                                            CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                SOPTWARE: FASTSEQ for Windows Version LENGTH: 767677
                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17361, Appropriate No. 6812339
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12147
LENGTH: 767677
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Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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ORGANISM: Human
FEATURE:
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LOCATION: (1)...(767677)
OTHER INFORMATION: n = A,T,C or G
ORGANISM: Human FEATURE:
                                             TYPE: DNA
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Local Similarity 51.4%;
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OF DETECTION AND USES THEREOF
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NAME/KEY: misc_feature

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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER FOR SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11786
LENGTH: 15108
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; OTHER INFORMATION: n = A
US-09-949-016-17361
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Sequence 17205, Application US/09949016
PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11786, Application US/09949016 Patent No. 6812339
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human
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Conservative
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Pred. No. 0.05; 
0; Mismatches 90; Indels 0
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OF DETECTION AND USES
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PELICATION NUMBER: 60/237,768
PRIOR PELICATION NUMBER: 60/237,768
PRIOR PELICATION NUMBER: 60/231,498
PRIOR PELICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEO ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.
SEQ ID NO 17205
LENGTH: 15108
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Matches
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CURRENT APPLICATION NUMBER: US/09/845,583A

CURRENT FILING DATE: 2001-04-30

PRIOR APPLICATION NUMBER: US 60/200,863

PRIOR FILING DATE: 2000-05-01

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Brunken, William Joseph
APPLICANT: Champliaud, Marie-France
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TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
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CCTGTGGTCCCTGGCTGGCAGTGACACTGACCGCTCTGAG 6005
                                                                 TTCCTGGACTCTGGCCCCCAGTGTACATGGGCGCACGGGG 168
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llarity 52.5%;
Conservative
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RESULT 11 US-09-949-016-12957 ; Sequence 12957, Application US/09949016 ; Patent No. 6812339

GENERAL INFORMATION:

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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                    ; ORGANISM: Human
US-09-949-016-12208
                                                                            Query Match
Best Local Similarity
Matches 92; Conserv
                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRBtSEQ for Windows Version
SEQ ID NO 12208
LENGTH: 30244
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SEQ ID NO 12957
LENGTH: 35471
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Best Local
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NAME/KEY: misc_feature

LOCATION: (1)...(35471)

OTHER INFORMATION: n = A,T,C or

1-09-949-016-12957
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                              TYPE: DNA
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13568 GCCAGCTGTACATCTGGGTGCTCTGGGGACCCGGGCGTTCACGGCATGTTGCCCTGGGT 13627
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                                       40 GCCCCCAGTGTACATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGT 99
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                                                                                 Conservative
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55.4%;
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                                                                                                Score 36.8; DB Pred. No. 0.28;
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                                                                                 Mismatches
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OF DETECTION
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OF DETECTION AND USES THEREOF
                                                                                                                      Length 30244;
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US-09-949-016-13550
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US-09-949-016-13550
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SOFTWARE: PER
SEQ ID NO 138
LENGTH: 3054
                                                                                                                                                                                                                                                                  Sequence 138, Application US/09484970B Patent No. 6426186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 13550
LENGTH: 30245
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                                                              APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
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nes 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                          13686
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                                                                                                                                                                                                                                                                                                                                                                                                          TGCTCTGGGGACCCGGGTGGTTCATGGCATGTTGCCCCTGGGTTTTT 13731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTCCAGGGACCCGGGCGGTTTGTGGGCATGGCT - - ACAGCAGCCAGCTGTACATCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCACGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTAT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCAGCTGTACATCTGGGTGCTCTGGGGACCCGGGCGGTTCACGGCATGTTGCCCTGGGT 13627
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                                           PERL Program
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55.4%;
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TYPE: DNA
ORGANISM: Homo

sapiens

NAME/KEY: misc_feature OTHER INFORMATION: Incyte ID

No. 6426186 336987.1CB1

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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTEN, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

VUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13841

LENGTH: 134008

TYPE: DNA

ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:

NAME/KEY: misc_feature

; LOCATION: (1)...(134008)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-13841
Search completed: September Job time: 139.759 secs
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US-09-949-016-13841
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                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 57; Conserv
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                                                                                                                                                                                        95 CCAGTGTACATGGGGGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTAC 154
                                                                                                                                                                                                                                                                       35 CTCTGGCCCCAGTGTACATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCC 94
                                                                                                                                                                                                                                                                                                              85;
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                                                                             CTGGACGCACGACGACGTGGACGCACGGATGACTCAGATCCCCAG 127237
                                                                                                                 ATGGGCGCACGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCAG 200
                                                                                                                                                                                                                                   CACGGACACCCAGACGACGCGCACAGACGACGCGCGCACGCACAGATGACGTGGACGC 127131
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                2005, 07:07:22
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                                                                                                                                                                                                                                                                                                                                Score 36.4; DB 4; Length 134008; Pred. No. 0.74;
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